PERFORMANCE EVALUATION OF DS-CDMA RECEIVERS USING GENETIC ALGORITHM

A THESIS SUBMITTED IN PARTIAL FULFILLMENT
OF THE REQUIREMENTS FOR THE DEGREE OF

Master of Technology
In
Telematics & Signal Processing

By
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Roll no :20607028

Department of Electronics & Communication Engineering
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CERTIFICATE

This is to certify that the Thesis Report entitled **"*Performance evaluation of DS-CDMA receiver using genetic algorithm* "** submitted by Mr. **Prasanta Kumar Pradhan (20607028)** in partial fulfillment of the requirements for the award of Master of Technology degree in Electronics and Communication Engineering with specialization in "Telematics & Signal processing " during session 2007-2008 at National Institute Of Technology, Rourkela (Deemed University) and is an authentic work by him under my supervision and guidance.To the best of my knowledge, the matter embodied in the thesis has not been submitted to any other university/institute for the award of any Degree or Diploma.

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CONTENTS

ABSTRACT

Direct sequence-code division multiple access (DS-CDMA) technique is used in cellular systems where users in the cell are separated from each other with their unique spreading codes. In recent times DS-CDMA has been used extensively. These systems suffers from multiple access interference (MAI) due to other users transmitting in the cell, channel inter symbol interference (ISI) due to multipath nature of channels in presence of additive white Gaussian noise(AWGN). Spreading codes play an important role in multiple access capacity of DS-CDMA system. M-sequences, gold sequences etc., has been traditionally used as spreading codes in DS-CDMA. These sequences are generated by shift registers and periodic in nature. So these sequences are less in number and also limits the security.

This thesis presents an investigation on use of new type of DS CDMA receiver called Genetic Algorithm based DS-CDMA receiver. Genetic Algorithm is robust optimization technique and does not fall into local minima hence this gives better weight optimization of any system. This Thesis investigates the performance of GA based DS-CDMA communication using gold code sequences.

Extensive simulation studies demonstrate the performance of the different linear and nonlinear DS-CDMA receivers like RAKE receiver, matched filter (MF) receiver, minimum mean square error (MMSE) receiver using gold sequences and the performance have been compared with GA based receiver.

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ACRONYMS AND ABBREVIATIONS

AWGN	additive white Gaussian noise
BER	bit error ratio
BPSK	binary phase shift keying
CDMA	code division multiple access
CIR	carrier to interference ratio
CLB	chip level based
DS	direct sequence
FIR	finite impulse response
FLANN	Functional link artificial neural network
GA	Genetic algorithm
ISI	inter symbol interference
LMS	least mean square
LOS	line of sight
LPI	low probability of interception
MAI	multiple access interference
MF	matched filter
MMSE	minimum mean square error
MUD	multi user detection
PG	processing gain
PPB	preprocessing based
PN	pseudonoise
PSD	power spectral density
RLS	recursive least square
SNR	signal to noise ratio
SS	spread spectrum
SSMA	spread spectrum multiple access
TDL	tapped-delay-line

NOMENCLATURE

f_{chip}	chip frequency
T_{bit}	bit period
x (n)	data bits
M	length of spreading sequence
$S_D(f)$	Power spectral density of the original unspread signal
$S_{SS}(f)$	Power spectral density of the spreading sequence
g_P	Processing gain
W_{SS}	Bandwidth of spread signal
W_D	Bandwidth of Data signal
T_{chip}	chip time period
σ^2	Noise power
$s(kL+n)$	transmitted signal
$C_{i,n}$	ith bit of nth user
$x_i(k)$	data bit of ith user
f_0	coherence bandwidth
T_0	coherence time
$S(\tau)$	multipath intensity profile
$\underline{y}(n)$	received signal vector
ω	Tap weight vector
$\tilde{x}(n)$	soft output
$\hat{x}(n)$	hard estimate
L	tap weights
F	transformation mapping function
r	bifurcation parameter

C_k	Binary sequences
C_d	Spreading sequence vector of the desired user d
$\hat{D}$	The estimated transmitted bit of the desired user *d*
y	received signal
H_{ch}	multipath channel
f_{Pen}	penalty function,
N_{train}	number of training bits
e(k)	the error associated with filter output y(k).
μ	Step size
$v(kN+n)$	output for the kth symbol of length N with n
$y(kN+n)$	The filter input

Chapter 1

INTRODUCTION

1.1 INTRODUCTION

Spread spectrum techniques have been wildly used in wired and wireless communications. The spreading of the signal spectrum gives us many advantages such as robustness against interference and noise, low probability of intercept, realization of Code Division Multiple Access(CDMA) and so on. In order to spread the bandwidth of the transmitting signals, pseudo-noise (PN) sequences have been used extensively in spread-spectrum communication systems [1]. Obviously, the maximal length shift register sequences (M-sequences) and Gold sequences are the most popular spreading sequences in spread spectrum systems. Many other codes like Walsh code and Chaotic code were reported for the better performance of the CDMA system.

At the receiver end we extract the spreading code in order to retrieve the data from the received noisy signal. This code extraction is done by means of the adaptive channel equalization. Many type of channel equalization techniques like Least Mean Square(LMS),Recursive Least Square(RLS),Decision Feedback Equalizer(DFE) and so on were reported for the code extraction of the CDMA system. All the equalization methods mentioned above are gradient based algorithms. So they suffer from the so called problem in channel equalization local minima. Hence they stick around the local minima and never fall into the global minima. Again the above mentioned equalization techniques are not able to handle the nonlinearity associated with a channel.

To overcome the local minima problem many evolutionary computing methods such as Genetic Algorithm (GA), Particle Swarm Optimization (PSO), Bacteria Foraging Optimization (BFO) were proposed .As being these techniques are nongradient based algorithm they completely search the search space and fall into the global minima never to the local minima. In this thesis we will use GA based channel equalization to improve the performance of the CDMA system.

The chapter begins with an exposition of the principal motivation behind the work undertaken in this thesis. Following this, section 1.3 provides a brief literature survey on GA. Section 1.4 outlines the contributions made in this thesis. At the end, section 1.5 presents the thesis layout.

1.2 MOTIVATION OF WORK

In order to spread the bandwidth of the transmitting signals, the binary pseudo-noise (PN) sequences[3] have been used extensively in spread spectrum communication (SS) systems. It is a deterministic, periodic signal that is known to both transmitter and receiver,

whose appearance has the statistical properties of sampled white noise. It appears, to an unauthorized listener, to be a similar to those of white noise. Therefore, it is not easily intercepted by adversary.

Much research has been done over the past decades in order to analyze the properties of these sequences and to try to find easier ways to generate the most effective codes. Obviously, the maximal length shift register sequences (M-sequences) and Gold sequences are the most popular spreading sequences in spread spectrum systems. The M-sequences are the longest codes that can be generated with given a shift register of fixed length, that have relatively smaller cross-correlation values than the peak magnitude that restrict regretfully to their number. The m-sequences have very desirable autocorrelation properties. However, large spikes can be found in their cross-correlation functions, especially when partially correlated. Another limiting property of m-sequences is that they are relatively small in number. Therefore, the number of sequences is usually too small and not suitable for spread spectrum systems. Furthermore, another method for generating PN sequences with better periodic cross-correlation properties than M-sequence has been developed by Gold [4]. The Gold sequences are constructed by taking a pair of specially selected M-sequences.

In this thesis we used Gold sequences to evaluate the performance of DS CDMA system. As channel equalization is an important aspect in any communication technique so much work also has been carried out for equalization in the receiver. The simplest receiver structure for DS CDMA is matched filter which is the simplest correlation receiver with M tap weights. In a single user system, the matched filter is the optimum receiver for signals corrupted by only AWGN. In a multi user environment, however, the performance degrades rapidly with increasing number of users. The matched filter is multiple-access limited-and strong interferers with high power compared to the desired user cause severe problem. This latter effect is called the near-far problem. Due to these problems, other solution has been searched for. The optimal linear receiver for multi-user detection is MMSE receiver.

The motivation for the use of adaptive algorithms lies in the desire to change the individual taps of the receiver filter to respond to changes in the communication channel. The traditional implementation of adaptive receivers is that a sequence of a priori known training data is incorporated into the data stream at prearranged times. As the name suggests, the Minimum Mean Square Error (MMSE) detector minimizes the mean square error between the transmitted bit and the decision variable which is an output of the linear transformation. The detector circumvents the noise enhancement problem faced by the decorrelating detector.

However, the Minimum Mean Square Error (MMSE) detector minimizes the mean square error between the transmitted bit and the decision variable which is an output of the linear transformation. The detector circumvents the noise enhancement problem faced by the decorrelating detector. The linear transformation thus comprises of terms involving the received power levels and the thermal noise power. This detector offers improvement in BER performance, but a disadvantage is that received power levels have to be estimated. Erroneous estimations can lead to degradation of performance. As MMSE employs LMS or RLS algorithm so there is a chance of falling in local minima because LMS and RLS are gradient based algorithms. Some times communication channels are associated with some nonlinearity. But LMS and RLS are not robust to nonlinearity.

Many other methods using Artificial Neural Network (ANN), Radial Basis Function (RBF), Fuzzy Logic (etc.) were also investigated. The development of Evolutionary computation methods such as Genetic Algorithm (GA), Bacteria Foraging Optimization (BFO) and many other algorithms are challenging fields in machine learning and optimizing a system. In this thesis we have implemented GA for the performance evaluation of DS CDMA system.

1.3 BACKGROUND LITERATURE SURVEY

In the past few decades, there has been a great deal of interest in the study of evolutionary computing methods. Many evolutionary computing methods like Genetic Algorithm (GA),Bacteria Foraging optimization (BFO),Ant colony Optimization (ACO) and Particle Swarm Optimization (PSO) have been investigated.The genetic algorithm (GA) is an optimization and search technique based on the principles of genetics and natural selection. A GA allows a population composed of many individuals to evolve under specified selection rules to a state that maximizes the “fitness” (i.e., minimizes the cost function). The method was developed by John Holland (1975) over the course of the 1960s and 1970s and finally popularized by one of his students, David Goldberg, who was able to solve a difficult problem involving the control of gas-pipeline transmission for his dissertation (Goldberg,1989).Genetic algorithms are now widely applied in science and engineering as adaptive algorithms for solving practical problems. Certain classes of problem are particularly suited to being tackled using a GA based approach.

The general acceptance is that GAs are particularly suited to multidimensional global search problems where the search space potentially contains multiple local minima. Unlike other search methods, correlation between the search variables is not generally a problem. The basic GA does not require extensive knowledge of the search space, such as likely

solution bounds or functional derivatives. A task for which simple GAs are not suited is rapid local optimization; however, coupling the GA with other search techniques to overcome this problem is trivial. Whenever multidimensional systematic searching would be technique of choice, except that the large number of comparisons makes that approach intractable, a GA should be considered for the reasons outlined.

1.4 OBJECT OF THE WORK

The work proposed here intends to test the performance of DS-CDMA system using GA and compare the performance for other different receiver techjniques. This thesis presents an investigation on use of GA on DS CDMA system. In this work it is proposed to carry out the following studies.Implementation of Genetic Algorithm for the DS-CDMA downlink receiver.Investigate BER performance of different linear and nonlinear receivers for DS-CDMA system and compare the same using GA with gold sequences.

1.5 THESIS OUTLINE

This thesis is organized into six chapters. Following this introduction, Chapter 2 provides a more detail discuss on DS-CDMA system. Chapter 3 discusses the background of Genetic Algorithm. In Chapter 4, various linear receivers like Matched filter, MMSE receiver etc., are studied and BER performance of different linear receivers using gold sequences is evaluated and it is compared with the receivers using GA with gold sequences. Finally Chapter 5 provides concluding remarks and future work.

Chapter 2

DS-CDMA SYSTEM AND OVERVIEW

2.1 INTRODUCTION

In this section the principle of spread spectrum and its application in multiple access is discussed. Multiple access schemes are used to allow many mobile users to share simultaneously a finite amount of radio channels in a fixed radio spectrum. The sharing of the spectrum is required to achieve high capacity by simultaneously allocating the available bandwidth to multiple users.

Following this introduction, spread spectrum (SS) communication technique is discussed in the section 2.2. The application of this SS technique to produce a multiple access system is described in the section 2.3. The section 2.4 deals with the construction of a simplified form of a baseband signal to be transmitted, while section 2.5 considers the effects of multipath channel on this signal. Section 2.6 discusses the simplest receiver structure using matched filter (MF). Principle structure of multiuser detector is described in section 2.7. While generation of Gold sequence is discussed in section 2.8 and the chapter ends with the concluding remark.

2.2 SPREAD SPECTRUM COMMUNICATION TECHNIQUES

As a simple, expansion of the bandwidth is not sufficient to be termed as the spread spectrum, but the bandwidth expansion must be accomplished with the separate signature, or known as spreading sequence. Both transmitter and the receiver know this spreading sequence. It is also independent of the data bits [8]. All the sequences are randomly distributed, and there is no correlation between any two sequences.

Let the sequence of data bits x (n) have the period T_{bit} and the spreading sequence of length M (in this work we have taken a spreading sequence of length 31) generally called chips to distinguish them from the data bits have the frequency f_{chip} where $f_{chip} >> (1/T_{bit})$. In other words it is assumed that $f_{chip} >> f_{bit}$.

From the above assumption that the transmitted data is random and independent, the power spectral density of the original unspread signal is given by [9]

$$S_D(f) = T_{bit}\left(\frac{\sin \pi fT_{bit}}{\pi fT_{bit}}\right)^2 \qquad (2.1)$$

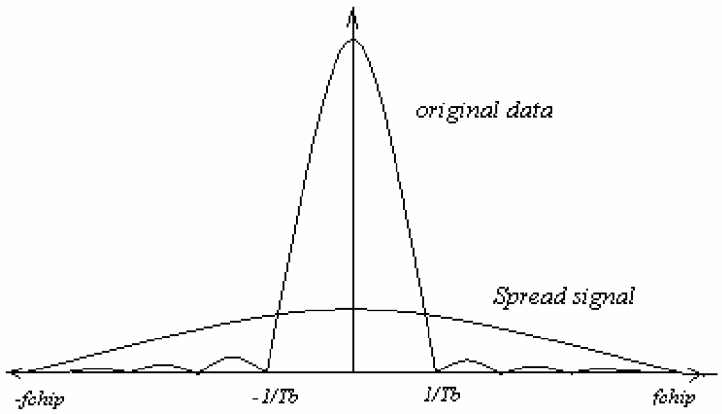


Figure 2.1: Spread spectrum concept in frequency domain

And assuming that spreading sequence is pseudorandom in nature, and is given by

$$S_{SS}(f) = \frac{1}{f_{chip}} \left(\frac{\sin \pi \ f / f_{chip}}{\pi \ f / f_{chip}} \right)^2 \qquad (2.2)$$

The relationship between the above spectral densities is sketched in the Figure 2.1.

The increased in performance due to the bandwidth expansion and contraction process is termed as processing gain g_P .This processing gain can be represented as the ratio of bandwidth associated with the spread signal W_{SS} and that of the data signal W_D.

$$g_P = \frac{W_{SS}}{W_D} = \frac{T_{bit}}{T_{chip}} \qquad (2.3)$$

The processing gain (PG) is normally expressed in decibel form as

$$G_P = 10 \log_{10} (g_P) \qquad (2.4)$$

The SS signal is largely tolerant to external interfering factors, there will be degradation in performance as the number of SS signals in the same cell increases.

. To make a good comparison, the background noise is expressed in terms of a modified form of signal to noise ratio (SNR), it takes account the processing gain.

$$\frac{E_b}{N_0} = 10 \log_{10} \left(g_P / 2\sigma^2 \right) \qquad (2.5)$$

Where E_b/N_0 is the signal to Gaussian noise ratio, and σ^2 is the Gaussian noise variance.

2.3 DS-CDMA TRANSMITTER PRINCIPLES

The simplest transmitter for downlink of a DS-CDMA is shown in the Figure 2.3. The transmitted signal $s(kL+n)$, at time $t = nT_{bit}$ is constructed by coherently summing the spreading sequence of each user, $C_{i,n}$ by that users bit $x_i(k)$ over all active users , to give

$$s(kL + n) = \sum_{i=1}^{U} C_{i,n}\, x_i(k) \qquad (2.6)$$

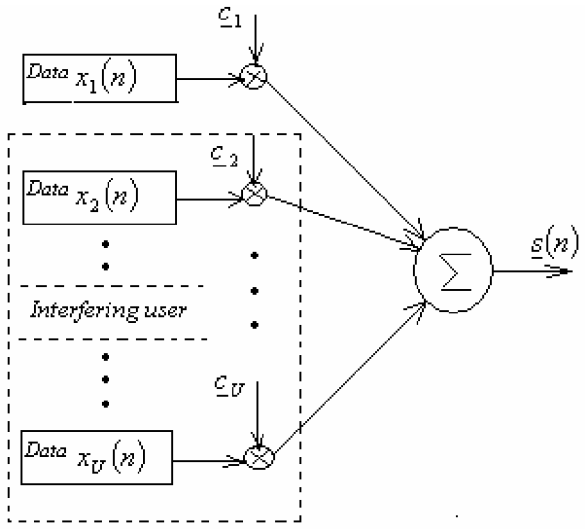


Figure 2.2: Simplified synchronous DS-CDMA downlink transmitters for U active users

In the uplink case the process is same except that the users are no longer synchronized, and which is modeled by inserting user-specific time delay on the resulting spread signal.

2.4 MULTIPATH CHANNEL BACKGROUND

The received signal consists of direct line of site (LOS) components and a few non LOS components. In addition to background noise, the received signal consists of a combination of individual reflected signals from the obstacles, like buildings etc, between the transmitter and the receiver and those arrives at various delays, according to the length of each associated RF paths [10]. This situation is called multipath channel. This is also time varying, due to the motion of the receiver with respect to the transmitter.

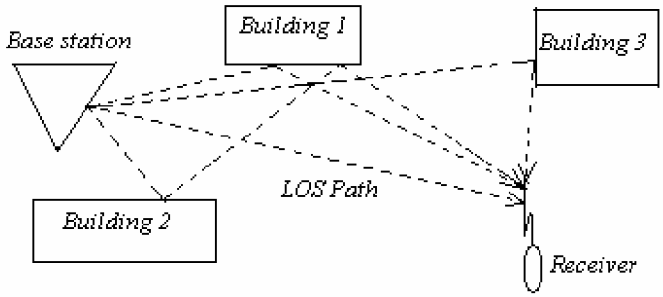


Figure 2.3: Example of multipath, the received signal consists of many reflections and delayed versions of the transmitted signal.

2.4.1 Channel effects

There are two main parameters of the channel, first is the range of frequency over which the channel effects remain same, called the coherence bandwidth, denoted as f_0, and the time duration over which the channel response is invariant is called the coherence time and denoted as T_0. These may be calculated from the two dual functions $S(\tau)$, the multipath intensity profile and $S(\nu)$, the Doppler power spectral density, which are the measure of the received signal power as the function of delay time τ and the Doppler shift ν respectively.

2.5 DS-CDMA RECEIVER PRINCIPLES

The work of the receiver is to recover the data x(n) by converting the spectrum of the received signal vector $\underline{y}(n)$. This is done by multiplying the received signal with the required spreading sequence, which is generated locally by the receiver. The received signal, consisting of M_r chips is passed to the block of delay elements, where Z^{-1} represents a delay of one chip, until the complete M_r chip signal has been read. These values are then passed to multiplier block in parallel, which forms the scalar product of $\underline{y}(n)$ and the tap weight vector $\underline{\omega} \in C^{M_r}$, where M_r is the number of tap weights, in this Figure 2.4 it is 8. This finite impulse response block produces a soft output $\tilde{x}(n)$, which is then passed through the decision block to give a hard estimate, $\hat{x}(n)$, of the original data bit x(n).

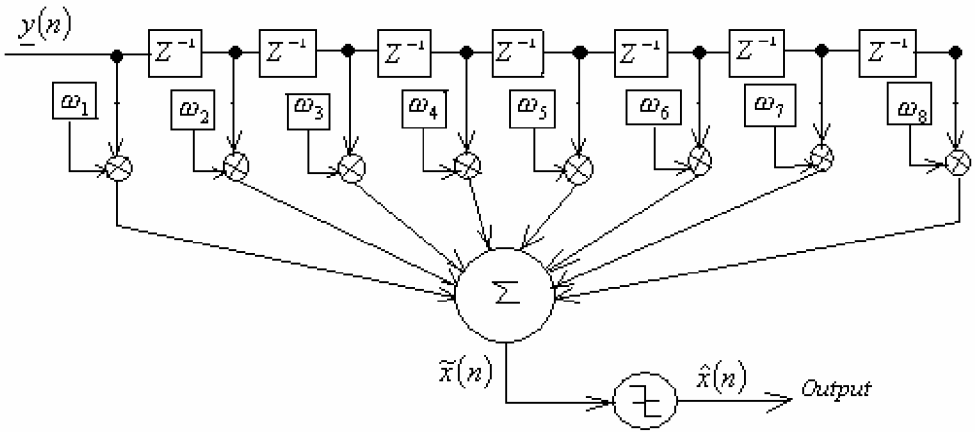


Figure 2.4: DS-CDMA correlator receiver with 8 tap weights

This is the structure of simplest receiver, commonly known as MF receiver with L tap weights $W_n : 1 \le n \le L$, matched to the original spreading sequence of the desired user. In practice, synchronization of the chip level signal is a highly non-trivial process. The performance of this receiver has been shown to degrade considerably as the number of simultaneously transmitting users increases . Hence improving the capacity of SS systems is achieved either by reducing the total interference by enhancing the single user detection methods or by making use of multiple access interference (MAI) through improved interference cancellation or multiuser detection technique (MUD).

2.6 PSEUDO NOISE (PN) DS/SS SYSTEM

Spread spectrum signals for digital communications were originally invented for military communication, but nowadays are used to provide reliable communication in a variety of commercial applications including mobile and wireless communications, which provide resistance to hostile jamming, hide the signal by transmitting it at low power, or make it possible for multiple users to communicate through the same channel. .In conventional DS/SS, in order to spread the bandwidth of the transmitting signals, the binary pseudo-noise (PN) sequences have been used extensively in spread spectrum communication (SS) systems. It is a deterministic, periodic signal that is known to both transmitter and receiver, whose appearance has the statistical properties of sampled white noise. It appears, to an unauthorized listener, to be a similar to those of white noise. Therefore, it is not easily intercepted by adversary.

The basic elements of a pseudo-noise DS/SS systems are illustrated in Figure 1 as the following.

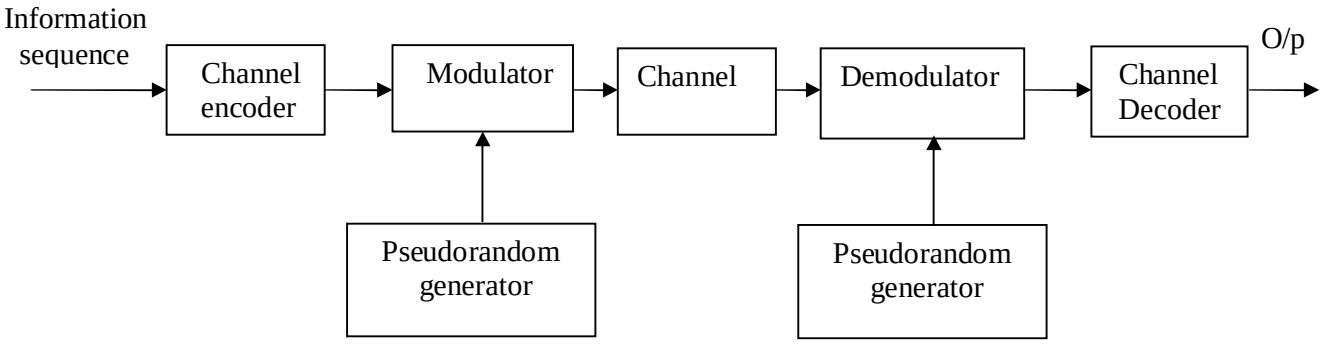


Figure 2.5 PN DS/SS system

The channel encoder and decoder, the modulator and demodulator are the basic elements of a conventional digital communication system. The two pseudorandom generators, interfacing with the modulator and demodulator, were employed by the spread spectrum system to produce a pseudorandom or pseudonoise (PN) binary-valued sequence that is used to spread the transmitted signal in frequency at the modular and to despread the received signal at the demodulator.

2.7 PSEUDO-RANDOM SEQUENCES

A pseudorandom(PN) sequence is a code sequence of 1's and 0's whose autocorrelation has properties similar to those of white noise. Some of the popular PN sequences are Maximal length shift register sequences(m-sequences), gold sequences etc.,

2.7.1 Maximal length shift register Sequence (m-sequence)

Maximal length shift register sequences are by definition, the longest codes that can be generated by a given shift register or a delay element of a given length. In binary shift register sequence generators, the maximum length sequence is 2^n-1 chips, where n is the number of stages in the shift register. A shift register sequence generator consists of a shift register working in conjunction with appropriate logic, which feeds back a logical combination of the state of two or more of its stages to input. The output of a sequence generator, and the contents of its n stages at any sample (clock) time, is a function of the outputs of the stages

Number Of Stages	Code Length	Maximal Taps
2	3	[2,1]
3	7	[3,1]
4	15	[4,1]
5	31	[5,2][5,4,3,2][5,4,2,1]
6	63	[6,1][6,5,2,1][6,5,3,2]
7	127	[7,1][7,3][7,3,2,1][7,4,3,2] [7,6,4,2][7,6,3,1][7,6,5,2][7,6,5,4,2,1][7,5,4,3,2,1]
8	255	[8,4,3,2][8,6,5,3][8,6,5,2] [8,5,3,1][8,6,5,2][8,7,6,1] [8,7,6,5,2,1][8,6,4,3,2,1]
9	511	[9,4][9,6,4,3][9,8,5,4][9,8,4,1] [9,5,3,2][9,8,6,5][9,8,7,2] [9,6,5,4,2,1][9,7,6,4,3,1] [9,8,7,6,5,3]
10	1023	[10,3][10,8,3,2][10,4,3,1][10,8,5,1] [10,8,5,4][10,9,4,1][10,8,4,3] [10,5,3,2][10,5,2,1][10,9,4,2]
11	2047	[11,1][11,8,5,2][11,7,3,2][11,5,3,5] [11,10,3,2][11,6,5,1][11,5,3,1] [11,9,4,1][11,8,6,2][11,9,8,3]
12	4095	[12,6,4,1][12,9,3,2][12,11,10,5,2,1] [12,11,6,4,2,1][12,11,9,7,6,5] [12,11,9,5,3,1][12,11,9,8,7,4] [12,11,9,7,6,][12,9,8,3,2,1] [12,10,9,8,6,2]
13	8191	[13,4,3,1][13,10,9,7,5,4] [13,11,8,7,4,1][13,12,8,7,6,5] [13,9,8,7,5,1][13,12,6,5,4,3] [13,12,11,9,5,3][13,12,11,5,2,1] [13,12,9,8,4,2][13,8,7,4,3,2]
14	16,383	[14,12,2,1][14,13,4,2][14,13,11,9] [14,10,6,1][14,11,6,1][14,12,11,1] [14,6,4,2][14,11,9,6,5,2] [14,13,6,5,3,1][14,13,12,8,4,1] [14,8,7,6,4,2][14,10,6,5,4,1] [14,13,12,7,6,3][14,13,11,10,8,3]
15	32,767	[15,13,10,9][15,13,10,1][15,14,9,2] [15,1][15,9,4,1][15,12,3,1][15,10,5,4] [15,10,5,4,3,2][15,11,7,6,2,1] [15,7,6,3,2,1][15,10,9,8,5,3] [15,12,5,4,3,2][15,10,8,7,5,3] [15,13,12,10][15,13,10,2][15,12,9,1] [15,14,12,2][15,13,9,6][15,7,4,1] [15,4][15,13,7,4]

Table 2.1: Feedback connections for linear m-sequences

fed back at the preceding sample time. Feedback connections have been tabulated for maximal code generators for 3 to 15 stages and listed in Table 3.1.

Implementation

Linear feedback shift registers (LFSR) can be implemented in two ways. The Fibonacci implementation consists of a simple shift register in which a binary-weighted modulo-2 sum of the taps is fed back to the input. (The modulo-2 sum of two 1-bit binary numbers yields 0 if the two numbers are identical and 1 if they differ: 0+0=0, 0+1=1, 1+1=0.)

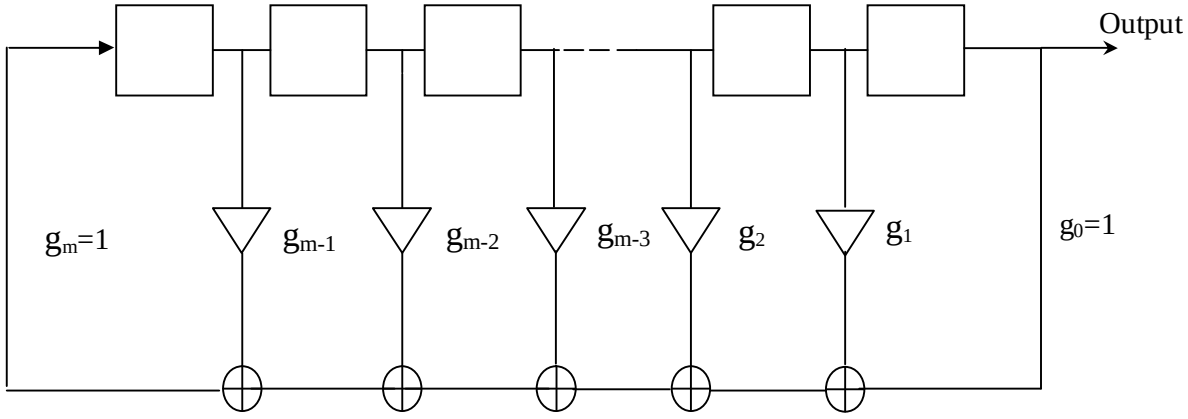


Figure 2.6: Fibonacci implementation of LFSR

For any given tap, weight g_i is either 0, meaning "no connection," or 1, meaning it is fed back. Two exceptions are g_0 and g_m, which are always 1 and thus always connected. Note that g_m is not really a feedback connection, but rather is the input of the shift register. It is assigned a feedback weight for mathematical purposes. The Galois implementation consists of a shift register, the contents of which are modified at every step by a binary-weighted value of the output stage.

2.7.2 Gold sequences

For CDMA applications, m-sequences are not optimal. For CDMA, we need to construct a family of spreading sequences, one for each which, in which the codes have well-defined cross-correlation properties. In general, m-sequences do not satisfy the criterion. One popular set of sequences that does are the Gold sequences. Gold sequences are attractive because only simple circuitry is needed to generate a large number of unique codes.

A Gold sequence is constructed by the XOR of two m-sequences with the same clocking. Figure 2.7 shows the schematic for Gold code generation.

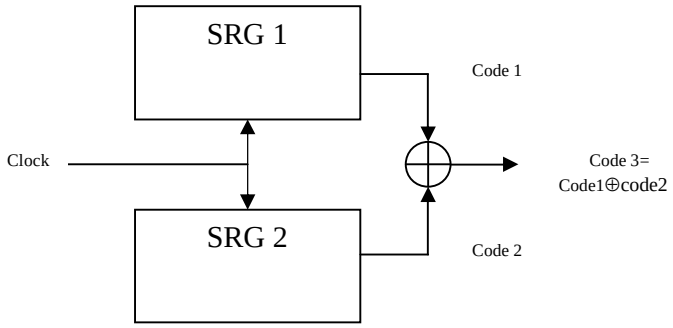


Figure 2.7: Gold code sequence generator configuration

To achieve increased capacity, at an expense of altering the correlation properties slightly, a pair of m-sequences may be used to generate a set of Gold sequence , which have the property that the cross-correlation is always equal to –1, when the phase offset is zero. Non-zero phase offset produces a correlation value from one of the three possible values. In this work a pair of specially selected m-sequences (where m = 5) is taken, and performing the modulo-2 sum of the two sequences for each of the $L=2^m-1$ cyclically shifted version of one sequence relative to the other sequence. Thus L Gold sequence is generated as illustrated in Figure 2.8.

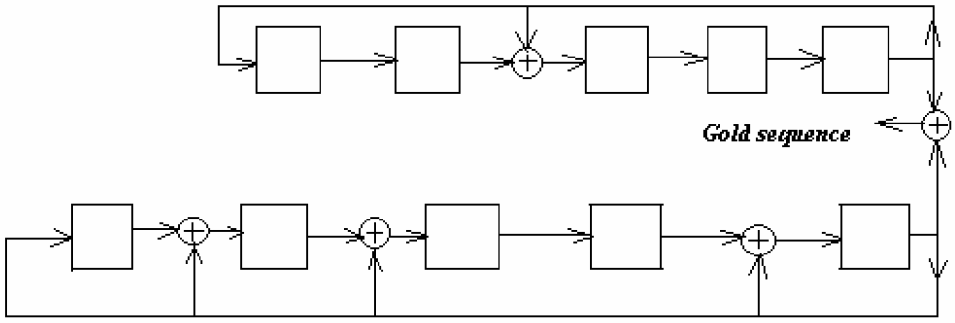


Figure 2.8 Generation of Gold sequences of length 31

In this section we discussed about the basic principles of SS communication and implementation of the DS-CDMA. The transmitter and receiver structure have been discussed. In this section we also reviewed the Gold sequence generation. By far, the maximum-length shift-register sequences (*m*-sequence) are the most widely known binary PN code sequences. The most undesirable property of m-sequence is that they are relatively small in number. For example, for a sequence of *N=63*, there are only 6, and for *N=255*, there are only 16 possible different sequences to use. Therefore, m-sequences are not suitable for PN DS/SS systems.

A generation of Pseudo-noise is core for spread spectrum systems. The classical M-sequences and Gold sequences are not suitable, since their number and security is not friendly to DS-SS systems.

2.8 CONCLUSION

This chapter reviewed the basic principles of SS communications and described the implementational aspects of DS-CDMA. The simplified transmitter structure for downlink scenario has been outlined, the model for communication channel is introduced. Simplest chip level processed MF receiver has been discussed in brief. Process of generation of 31 chip Gold sequence was described at the end.

Chapter 3

INTRODUCTION TO GENETIC ALGORITHM

3.1 INTRODUCTION

The genetic algorithm (GA) is an optimization and search technique based on the principles of genetics and natural selection. A GA allows a population composed of many individuals to evolve under specified selection rules to a state that maximizes the "fitness" (i.e., minimizes the cost function). The method was developed by John Holland (1975) over the course of the 1960s and 1970s and finally popularized by one of his students, David Goldberg, who was able to solve a difficult problem involving the control of gas-pipeline transmission for his dissertation (Goldberg,1989).

Some of the advantages of a GA include that it

i. Optimizes with continuous or discrete variables,
ii. Doesn't require derivative information,
iii. Simultaneously searches from a wide sampling of the cost surface,
Iv.Deals with a large number of variables,
v. Is well suited for parallel computers,
vi. Optimizes variables with extremely complex cost surfaces (they can jump out of a local minimum),
vii. Provides a list of optimum variables, not just a single solution,
May encode the variables so that the optimization is done with the encoded variables, and Works with numerically generated data, experimental data, or analytical functions.

These advantages are intriguing and produce stunning results when traditional optimization approaches fail miserably.

3.1.1 Evolutionary Computation

It is an appealing idea that the natural concepts of evolution may be borrowed for use as a computational optimization tool. A family of algorithms has been developed around this idea:

- evolution strategies (ES)
- evolutionary programming (EP)
- genetic algorithms (GA)
- genetic programming (GP)

The fundamentals of genetic algorithms will be introduced in this section. It should be highlighted that these evolutionary algorithms are not random searches for a very fit

individuals (i.e. the solutions to problems). Evolutionary algorithms use stochastic processes to produce a search behavior which is much better than random[4].

3.1.2 Genetic Algorithms for search and optimization

Genetic algorithms are now widely applied in science and engineering as adaptive algorithms for solving practical problems. Certain classes of problem are particularly suited to being tackled using a GA based approach.

The general acceptance is that GAs are particularly suited to multidimensional global search problems where the search space potentially contains multiple local minima. Unlike other search methods, correlation between the search variables is not generally a problem. The basic GA does not require extensive knowledge of the search space, such as likely solution bounds or functional derivatives. A task for which simple GAs are not suited is rapid local optimization; however, coupling the GA with other search techniques to overcome this problem is trivial. Whenever multidimensional systematic searching would be technique of choice, except that the large number of comparisons makes that approach intractable, a GA should be considered for the reasons outlined in the sections below.

GAs were first introduced by John Holland for the formal investigation of the mechanisms of natural adaptation (Holland 1975), but the algorithms have been since modified to solve computational search problems. Modern GAs deviate greatly from the original form proposed by Holland, but their linage is clear. There is no single firm definition for a genetic algorithm, and the computational system is highly simplified compared to the actual situation in nature. Therefore, we must first define a few terms and show how they relate between modern GAs and more traditional evolutionary theory.

GAs are broadly classified into two categories. They are

1. Binary GA
2. Contineous GA

In our application we are using binary GA.

3.2 COMPONENTS OF BINARY GENETIC ALGORITHM:

The GA begins, like any other optimization algorithm, by defining the optimization variables, the cost function, and the cost. It ends like other optimization algorithms too, by testing for convergence. In between, however, this algorithm is quite different. A path through the components of the GA is shown as a flowchart in Figure 3.1 .Each block in this “big picture” overview is discussed in detail in this chapter.

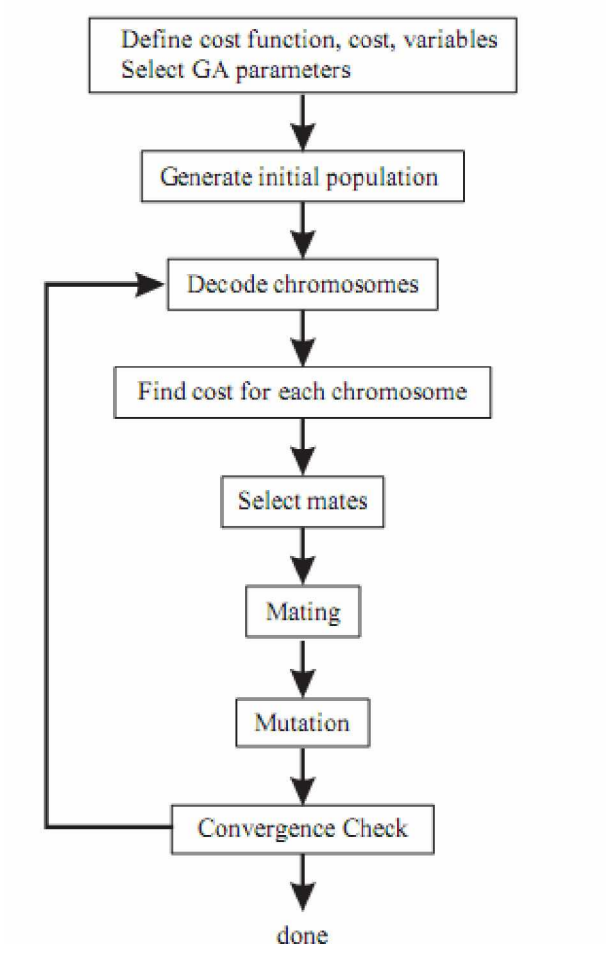


Fig 3.1 Flowchart of a binary GA

3.2.1 Selecting the Variables and the Cost Function

A cost function generates an output from a set of input variables (a chromo- some). The cost function may be a mathematical function, an experiment, or a game. The object is to modify the output in some desirable fashion by finding the appropriate values for the input variables. We do this without thinking when filling a bathtub with water. The cost is the difference between the desired and actual temperatures of the water. The input variables are how much the hot and cold spigots are turned. In this case the cost function is the experimental result from sticking your hand in the water. So we see that deter- mining an appropriate cost function and deciding which variables to use are intimately related. The term fitness is extensively used to designate the output of the objective function in the GA literature. Fitness implies a maximization problem. Although fitness has a closer association with biology than the term cost, we have adopted the term cost, since most of the optimization literature deals with minimization, hence cost. They are equivalent. The GA begins by defining a chromosome or an array of variable values to be optimized. If the chromosome has N_{var}

variables (an N_{var}-dimensional optimization problem) given by P_1 ,P_2 ,P_3 ,….P_{Nvar} then the chromosome is written as an N_{var} element row vector.

$$Chromosome = [P_1 ,P_2 ,P_{3,}\ldots.,P_{Nvar}] \qquad (3.1)$$

For instance, searching for the maximum elevation on a topographical map requires a cost function with input variables of longitude (x) and latitude (y)

$$Chromosome =[x,y] \qquad (3.2)$$

Where N_{var} =2.Each chromosome has a cost found by evaluating the cost function, f, at $P_{1,}$ $P_{2,}$ $P_{3,\ldots}$ P_{Nvar};

$$cost =f(chromosome) = f(P_1 ,P_{2,\ldots.}\ P_{Nvar}) \qquad (3.3)$$

Putative solutions to the target problem are evaluated using "Cost functions", otherwise known as "Objective functions". Based upon the result of such functions, evolutionary pressures may be applied to a set of solutions. The objective function will obviously be problem specific, but there are certain features which should be avoided for the effective application of a GA. Such unfavorable objective functions are discussed below, but often the problems may be alleviated by choosing a different encoding scheme, by normalizing the input parameters, or by rebasing the function. An advantage of GAs over many search or optimization algorithms is that derivatives of this function are not required. This fact ensures that GAs may be readily applied on fitness landscapes (or potential surfaces) which contain discontinuities or singularities without any special treatments[5].

Often the cost function is quite complicated, as in maximizing the gas mileage of a car. The user must decide which variables of the problem are most important. Too many variables bog down the GA. Important variables for optimizing the gas mileage might include size of the car, size of the engine, and weight of the materials. Other variables, such as paint color and type of headlights, have little or no impact on the car gas mileage and should not be included. Sometimes the correct number and choice of variables comes from experience or trial optimization runs. Other times we have an analytical cost function[6]

3.2.2 Variable Encoding and Decoding

Since the variable values are represented in binary, there must be a way of converting continuous values into binary, and visa versa. Quantization samples a continuous range of values and categorizes the samples into nonoverlapping subranges. Then a unique discrete

value is assigned to each subrange.The difference between the actual function value and the quantization level is known as the quantization error. Quantization begins by sampling a function and placing the samples into equal quantization levels. Any value falling within one of the levels is set equal to the mid, high, or low value of that level. In general, setting the value to the mid value of the quantization level is best, because the largest error possible is half a level. Rounding the value to the low or high value of the level allows a maximum error equal to the quantization level. The mathematical formulas for the binary encoding and decoding of the *n*th variable are given as follows:

For encoding,

$$p_{norm} = \frac{p_n - p_{lo}}{p_{hi} - p_{lo}} \qquad (3.4)$$

$$gene[m] = round\{p_{norm} - 2^{-m} - \sum_{p=1}^{m-1} gene[p] * 2^{-p}\} \qquad (3.5)$$

For decoding

$$p_{quant} = \sum_{m=1}^{N_{gene}} gene[m] * 2^{-m} + 2^{-(m+1)} \qquad (3.6)$$

$$q_n = p_{quant}(p_{hi} - p_{lo} + p_{lo}) \qquad (3.7)$$

In each case

p_{norm} =normalized variable

p_{lo} =smallest variable value

p_{hi} =highest variable value

Gene[m]= binary version of p_n

Round{.} = round to nearest integer

p_{quant} =quantized version of p_{norm}

3.2.3 The Population

The GA starts with a group of chromosomes known as the population. The population has *Npop chromosomes* and is an N_{pop} * N_{pop} matrix filled with random ones and zeros generated using

Pop=round (rand (N_{pop} ,N_{bits}))

Where the function (N_{pop} ,N_{bits}) generates a (N_{pop} ,N_{bits}) matrix of uniform random numbers between zero and one. The function round rounds the numbers to the closest integer which in this case is either 0 or 1. Each row in the pop matrix is a chromosome. The chromosomes correspond to discrete values of longitude and latitude. Next the variables are passed to the cost function for evaluation.

3.2.4 Natural Selection

Survival of the fittest translates into discarding the chromosomes with the highest cost. First, the N_{pop} costs and associated chromosomes are ranked from lowest cost to highest cost. Then, only the best are selected to continue, while the rest are deleted. The selection rate, X_{rate} is the fraction of *Npop* that survives for the next step of mating. The number of chromosomes that are kept each generation is

$N_{keep} = X_{rate}\, N_{pop}$

Natural selection occurs each generation or iteration of the algorithm. Of the *Npop* chromosomes in a generation, only the top N_{keep} survive for mating, and the bottom

Npop – Nkeep are discarded to make room for the new offspring. Deciding how many chromosomes to keep is somewhat arbitrary. Letting only a few chromosomes survive to the next generation limits the available genes in the offspring. Keeping too many chromosomes allows bad performers a chance to contribute their traits to the next generation. We often keep 50% (X_{rate}= 0.5) in the natural selection process.

3.2.5 Selection

Now it's time to play matchmaker. Two chromosomes are selected from the mating pool of N_{keep} chromosomes to produce two new offspring. Pairing takes place in the mating population until N_{pop}-N_{keep} offspring are born to replace the discarded chromosomes. Pairing chromosomes in a GA can be as interesting and varied as pairing in an animal species.

GA selection operators perform the equivalent role to natural selection. The overall effect is to bias the gene set in following generations to those genes which belong to the most fit individuals in the current generation.

There are numerous selection schemes described in the literature; Roulette wheel selection, tournament selection, random selection, stochastic sampling. These, in essence, mimic the processes involved in natural selection.

1. Pairing from top to bottom: Start at the top of the list and pair the chromosomes two at a time until the top N_{keep} chromosomes are selected for mating. Thus, the algorithm pairs odd rows with even rows. The mother is row numbers in the population matrix given by *ma* = 1, 3, 5, … and the father has the row numbers pa = 2, 4, 6, …This approach doesn't model nature well but is very simple to program.

2. Random Pairing: This approach uses a uniform random number generator to select chromosomes. The row numbers of the parents are found using

$$ma = ceil(N_{keep} * rand(1, N_{keep}))$$

$$pa = ceil(N_{keep} * rand(1, N_{keep}))$$

Where *ceil* rounds the value to the next highest integer

3. Weighted random pairing: The probabilities assigned to the chromosomes in the mating pool are inversely proportional to their cost. A chromosome with the lowest cost has the greatest probability of mating, while the chromosome with the highest cost has the lowest probability of mating. A random number determines which chromosome is selected. This type of weighting is often referred to as roulette wheel weighting. There are two techniques: rank weighting and cost weighting.

a. Rank weighting. This approach is problem independent and finds the probability from the rank, *n*, of the chromosome:

$$p_n = \frac{N_{keep} - n + 1}{\sum_{n=1}^{N_{keep}} n}$$

Table 2.5 shows the results for the N_{keep} = 4 chromosomes. The cumulative probabilities listed in column 4 are used in selecting the chromosome. A random number between zero and one is generated.

Starting at the top of the list, the first chromosome with a cumulative probability that is greater than the random number is selected for mating pool. For instance, if the random number is r =.577, then $0.4 < r \leq 0.7$, so $chromosome_2$ is selected. If a chromosome is paired with itself, there are several alternatives. First, let it go. It just means there are three of these chromosomes in the next generation. Second, randomly pick another chromosome. The randomness in this approach is more indicative of nature. Third, pick another chromosome using the same weighting technique. Rank weighting is only slightly more difficult to program than the pairing from top to bottom. Small populations have a high probability of selecting the same chromosome.

The probabilities only have to be calculated once. We tend to use rank weighting because the probabilities don't change each generation.

n	Chromosome	P_n	$\sum_{i=1}^{n} P_i$
1	00110010001100	0.4	0.4
2	11101100000001	0.3	0.7
3	00101111001000	0.2	0.9
4	00101111000110	0.1	1.0

Table.3.1 Rank weighting

b. Cost weighting. The probability of selection is calculated from the cost of the chromosome rather than its rank in the population. A normalized cost is calculated for each chromosome by subtracting the lowest cost of the discarded chromosomes ($C_{N_{keep}+1}$) from the cost of all the chromosomes in the mating pool:

$$c_n = c_n - C_{N_{keep}}$$

Subtracting $C_{N_{keep}+1}$ ensures all the costs are negative. p_n is calculated from

$$p_n = \left| \frac{C_n}{\sum_{m}^{N_{keep}} C_m} \right|$$

This approach tends to weight the top chromosome more when there is a large spread in the cost between the top and bottom chromosome. On the other hand, it tends to weight the chromosomes evenly when all the chromosomes have approximately the same cost. The same issues apply as discussed above if a chromosome is selected to mate with itself. The probabilities must be recalculated each generation.

4. Tournament selection: Another approach that closely mimics mating competition in nature is to randomly pick a small subset of chromosomes (two or three) from the mating pool, and the chromosome with the lowest cost in this subset becomes a parent. The tournament repeats for every parent needed. Thresholding and tournament selection make a nice pair, because the population never needs to be sorted. Tournament selection works best for larger population sizes because sorting becomes time-consuming for large populations.

3.2.6 Mating.

Mating is the creation of one or more offspring from the parents selected in the pairing process. The genetic makeup of the population is limited by the current members of the population. The most common form of mating involves two parents that produce two

offspring (see Figure 3.2).A crossover point, or kinetochore, is randomly selected between the first and last bits of the parents' chromosomes. First, $parent_1$ passes its binary code to the left of that crossover point to $offspring_1$ In a like manner, $parent_2$ passes its binary code to the left of the same crossover point to $offspring_2$ .Next, the binary code to the right of the crossover point of $parent_1$ passes its code to $offspring_1$ goes to $offspring_2$ and $parent_2$ passes its code to $offspring_1$ .Consequently the offspring contain portions of the binary codes of both parents. The parents have produced a total of N_{pop}-N_{keep} offspring, so the chromosome population is now back to N_{pop}. Table 3.2 shows the pairing and mating process for the problem at hand. The first set of parents is chromosomes 3 and 2 and has a crossover point between bits 5 and 6. The second set of parents is chromosomes 3 and 4 and has a crossover point between bits 10 and 11. This process is known as simple or single-point crossover.

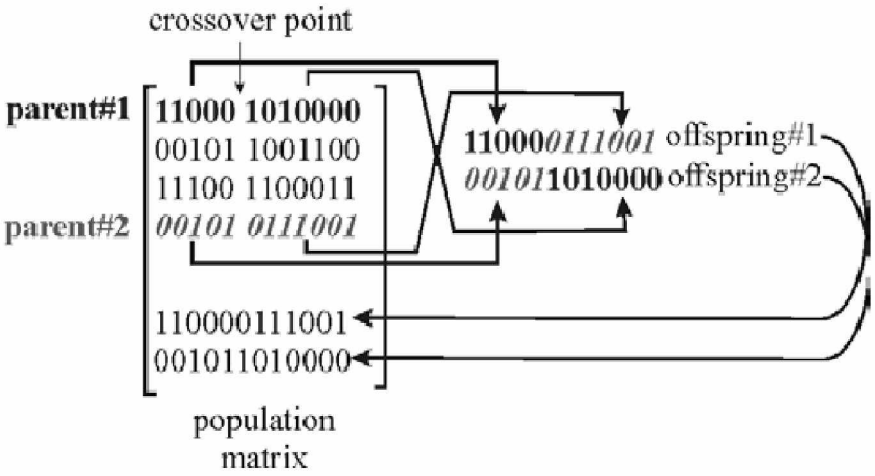


Fig 3.2 Two parents mate to produce two offspring

Chromosome	Family	Binary String
3	ma(1)	*00101111001000*
2	pa(1)	11101100000001
5	$offspring_1$	*00101*100000001
6	$offspring_2$	11101*111001000*
3	ma(2)	*00101111001000*
4	pa(2)	00101111000110
7	$offspring_3$	*00101111000*110
8	$offspring_4$	00101111001*000*

Table 3.2 Pairing and mating process of single point crossover

3.2.7 Mutations:

The exact purpose of the mutation operations depends upon who you talk to. Mutations enable the GA to maintain diversity whilst also introducing some random search behavior. As for crossover, many types of mutation operator may be conceived depending upon the details of the problem and the chromosomal representation of solutions to that problem.

Random mutations alter a certain percentage of the bits in the list of chromosomes. Mutation is the second way a GA explores a cost surface. It can introduce traits not in the original population and keeps the GA from con- verging too fast before sampling the entire cost surface. A single point mutation changes a 1 to a 0, and visa versa. Mutation points are randomly selected from the N_{pop} * N_{bits} total number of bits in the population matrix. Increasing the number of mutations increases the algorithm's freedom to search outside the current region of variable space. It also tends to distract the algorithm from converging on a popular solution. Mutations do not occur on the final iteration.

3.2.8 The Next Generation

After the mutations take place, the costs associated with the offspring and mutated chromosomes are calculated.

3.2.9 Convergence

The number of generations that evolve depends on whether an acceptable solution is reached or a set number of iterations is exceeded. After a while all the chromosomes and associated costs would become the same if it were not for mutations. At this point the algorithm should be stopped[7]

3.3 CONCLUSION

In this chapter the working of genetic algorithm is explained. As Ga searches the total search space so there is no chance to fall into local minima. Thus Genetic algorithms were able to accomplish both, evolving the system from a random arrangement to the near-perfect solution and finally to the perfect, optimal solution. At no step of the way did an insoluble difficulty or a gap that could not be bridged turn up. At no point whatsoever was human intervention required to assemble an irreducibly complex core of components (despite the fact that the finished product does contain such a thing) or to "guide" the evolving system over a difficult peak.

Chapter 4

PERFORMANCE OF LINEAR RECEIVERS FOR DS/SS SYSTEM

4.1 INTRODUCTION

A direct sequence code division multiple access (DS-CDMA) communications system receiver has three main obstacles to overcome. The first one is multiple access interference (MAI) from other users, which is a direct result of using DS-CDMA. In a cellular system, MAI will be non-stationary due to slow power variations caused by fading and it may undergo step changes when a new user starts or stops transmission (the birth or death of a signal).The transmission channel is responsible for the other two obstacles intersymbol interference caused by multipath and additive noise. To overcome these, many receiver structures have been proposed for the reception of DS-CDMA in a cellular environment.

This chapter reviews linear receiver structures for DS-CDMA.A brief overview of Linear receivers is given in section 4.1. Matched filter receiver is dicussed in section 4.2. MMSE receiver is discussed in section 4.3. In section 4.4 performance of different linear receivers like Matched filter, MMSE receiver and RAKE receiver using chaotic spreading sequences is investigated. The performance of nonlinear receivers using chaotic spreading codes is compared with that of gold sequences.

4.2 SINGLE USER RECEIVER

The task of the receiver is to recover the intended data *x(n)* by collapsing the spectrum of the received signal vector $\underline{y}(n)$. This is performed by integrating the product of the received signal with a locally held replica of the required user's spreading sequence. Practically, this is achieved by the correlator receiver, shown in Figure 4.1. The received signal, consisting of N_r chips is passed to the block of delay elements, where Z^{-1} represents a delay of one chip, until the complete N_r-chip signal has been read in.

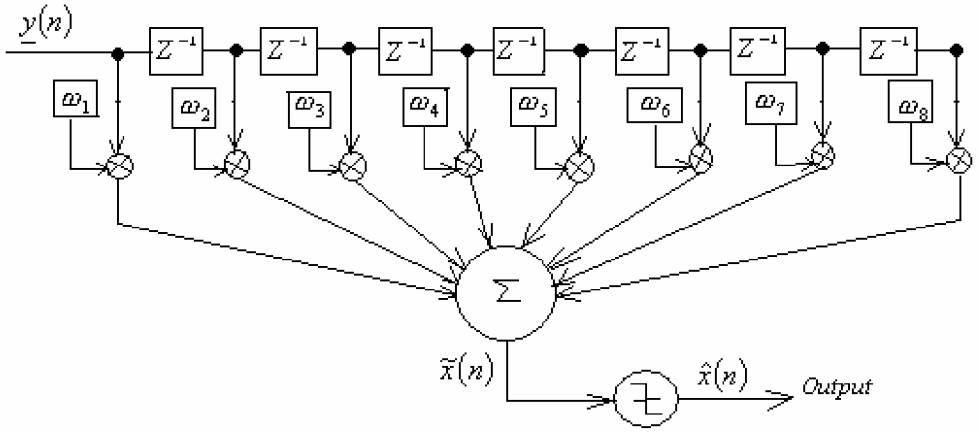


Figure 4.1: DS-CDMA correlator receiver with 8 tap delay.

These values are then passed in parallel to the multiplier block, which forms the scalar product of $\underline{y}(n)$ and the tap weight vector $\underline{w} \in C^{N_r}$ where N_r is the number of tap weights, which is set to 8 in the figure 4.1. This filter block produces a soft output, $\tilde{x}(n)$ which is then passed to the sign-decision block to give a hard estimate, $\hat{x}(n)$ of the original data bit, *x(n)* for the user of interest. Techniques to achieve synchronization involve the use of a pilot signal, which may be modeled by one additional user, whose data is constant. Perfect timing will be assumed in the following, except where stated.

4.3 MULTIUSER RECEIVER

Multiuser receivers[19] are a class of receivers that use knowledge of all the PN sequences to exploit the structure of the MAI. Instead of being separately estimated, as in a single user detection, the users are jointly detected for their mutual benefit. A CDMA receiver can either process the received signal at the chip rate or symbol rate (user bit rate).Figure 4.2 shows chip rate receivers, which consists of a bank of *matched filters* (MFs) or RAKEs. A bank of MFs is for the non-dispersive AWGN channel, whereas RAKEs[20] are considered for multipath channels. Current mobiles have a simple RAKE because of its simplicity, whereas base stations can have a bank of MFs (or RAKEs) as depicted in figures 4.2 and 4.3. However, structure Figure 4.2 suffers from MAI and therefore has limited performance. Performance improvement can be gained, when carrier to interference ratio (CIR) information from the interferers is taken into account to combat MAI, as structure in Figure 4.3 suggests. This structure is known as the *multiuser detector* (MUD) and is usually suggested for the asynchronous uplink receiver. It could also be used in a modified version as a single user detector in mobiles and might be implemented in the next generation of mobile systems.

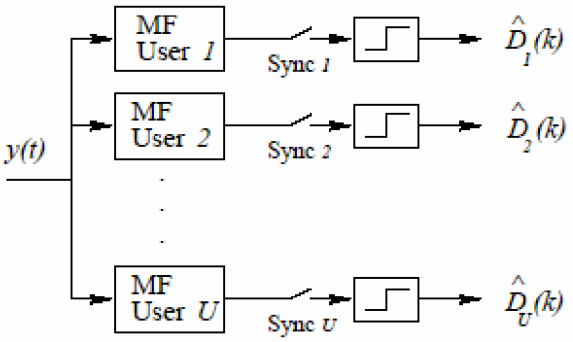


Figure 4.2: Conventional bank of single user receivers with MFs or RAKEs.

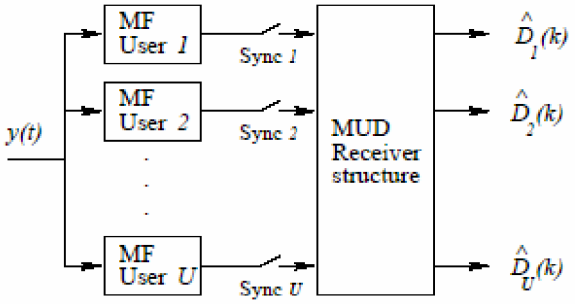


Figure 4.3: Verdu's proposed multiuser detector scheme with MFs for the AWGN channel.

A receiver structure which processes the received signal at the chip rate is known as a *chip level based* (CLB) receiver. Receivers, shown in Figure 4.3, which process at the symbol rate and consist of a front end bank of filters, will be called *preprocessing based* (PPB) receivers.

Because all optimum receivers are too complex for practical applications, the search for simpler and near optimum receivers became vital and goes on. Most proposals are based on the multiuser concept, which is preprocessing based (PPB) for several reasons. First, they relate to Verdu's MUD receiver, since they consider it optimum.

4.4 LINEAR RECEIVER

The general form of a linear receiver is given by $\hat{D} = \mathrm{sgn}(w^T.y)$ where the *sgn(.)* function returns the sign of the operand and where the filter weight vector **w** is chosen to minimize a cost function, while $\hat{D}$ is the estimated transmitted bit of the desired user *d* and **y** is the received signal, see Figure 4.4 and 4.5.

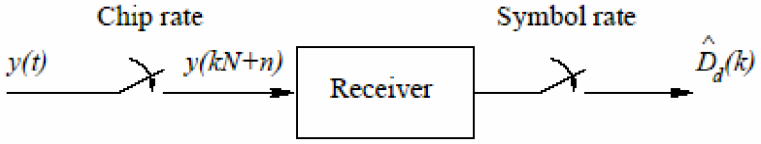


Figure 4.4: Chip rate based receiver.

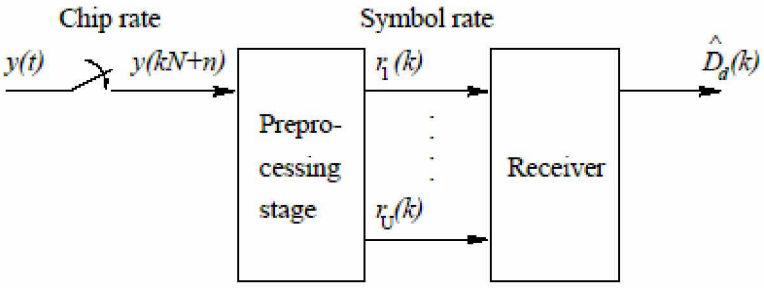


Figure 4.5: Symbol rate based receiver.

4.4.1 Matched Filter

The conceptually simplest receiver, the matched filter (MF) receiver, is simply the correlator receiver with M tap weights, $w_j : 1 \le j \le M$, matched to the complex conjugate time-reverse of the original spreading sequence of the required user which, without loss of generality, we may take to be user 1. The simplest CDMA receiver is the MF receiver, where w is replaced by Cd , the Spreading sequence vector of the desired user. In a multipath fading channel, w corresponds to the convolution between C_d and H_{ch}, implemented as a RAKE.

In practice, the acquisition and synchronization of the chip-level signal is a highly non-trivial task. A very simple and well known detector for SS signals is the matched filter detector, as shown in figure 4.6. The matched filter detector basically consists of a tapped-delay-line (TDL) filter of which the number of taps equals the spreading sequence length *N*. The output vector *(K)* of the tapped delay line $\underline{y}(k) = [y(k), y(k-1),..., y(k-N+1)]^T$ is multiplied with a vector of constant weight $\underline{w}$. $\underline{w} = [w_0, w_1,..., w_{N-1}]^T$. The resulting scalar product is applied to a decision function e.g. a s*ign* function. For the matched filter case, the weights w_k are matched to the user specific sequence code. $w_l = pn_u(N-1-l)$, *for* $0 \le l < N$. So that the matched filter output can be summarized as follows: $\tilde{D}(k) = \underline{w}^T . \underline{y}(k) = \sum_{l=0}^{N-1} w_l . y(k-l)$

Provided that the receiver is perfectly synchronized to the transmitter, the TDL extracts a set of chips that represents a particular sequence and the multiplication with the weights is equivalent to despreading operation. A following decision device such as s*ign* function leads

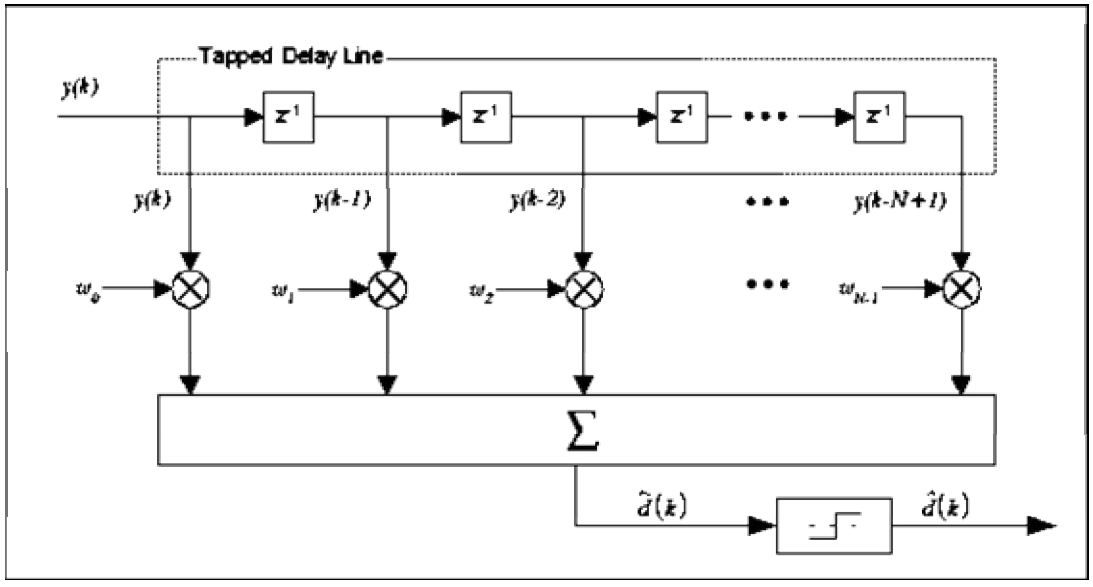


Figure 4.6: Matched filter

to the final estimate $\hat{D}(k)$ of the transmitted data bit *D(k)*, hence $\hat{D}(k) = \mathrm{sgn}\left(\tilde{D}(k)\right)$. The theoretical performance P_e of a MF receiver for a single cell system with *U* users, long random codes, where *N* is the number of chips (processing gain) in AWGN is:

$$P_e^{MF} = Q\left(\sqrt{\frac{N}{\sigma^2 + (U-1)}}\right), \qquad (4.1)$$

$$\text{where } Q(x) = 0.5 erfc\left(x/\sqrt{2}\right) \qquad (4.2)$$

and σ^2 denotes the noise power, derived from:

$$E_b/N_o = N/2\sigma^2 \qquad (4.3)$$

Where $\sigma^2 = N_o/2$ is the two sided noise power spectral density and E_b is the bit energy.

In a single user system, the matched filter is the optimum receiver for signals corrupted by only AWGN. In a multi user environment, however, the performance degrades rapidly with increasing number of users. The matched filter is multiple-access limited-and strong interferers with high power compared to the desired user cause severe problem. This latter effect is called the near-far problem. Due to these problems, other solution has been searched for. The optimal linear receiver for multi-user detection is MMSE receiver and is described in the next section.

4.4.2 MMSE receiver

The motivation for the use of adaptive algorithms lies in the desire to change the individual taps of the receiver filter to respond to changes in the communication channel. The traditional implementation of adaptive receivers is that a sequence of a priori known training data is incorporated into the data stream at prearranged times. It is important to acknowledge that this effectively reduces the overall data rate of the system, which is the main drawback of this approach.

The goal of any adaptive algorithm is to use this training data to force the receiver tap weights to minimize some cost or penalty function, $f_{Pen}(.)$, of the difference metric between the original data bit and its estimated value. The only requirement for this penalty function is that it be a monotonic increasing function of the absolute value of its argument, with a global minimum at zero. Here, the number of training bits is given by N_{train} and the sequence of training data by $\{x(n): 1 \leq n \leq N_{train}\}$.

MMSE receiver is an adaptive filter[21] as shown in Figure 4.7, in which the number of receiver tap weights Nr is set to length of the spreading code M.

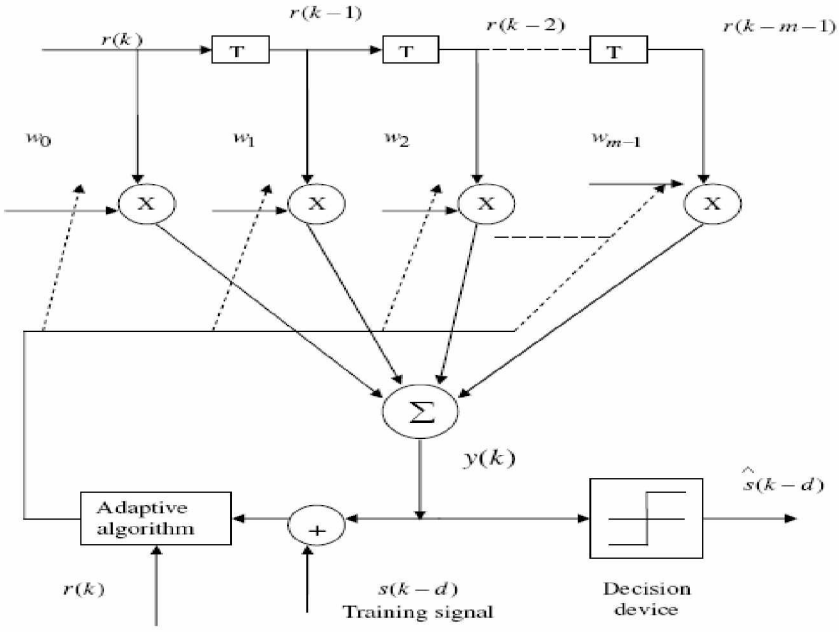


Figure 4.7 MMSE receiver

The MMSE criteria provide equalizer tap coefficients w(k) to minimize the mean square error at the equalizer output before the decision device. This condition can be represented as

$$J = \varepsilon | e(k) |^2 \qquad (4.4)$$

$$e(k) = s(k-d) - y(k) \qquad (4.5)$$

Where e(k) is the error associated with filter output y(k). However, the MMSE criteria optimize the equalizer weights for minimizing the MMSE under noise and ISI. Minimization of MMSE criteria provides equalizers that satisfy the Wiener criterion. The evaluation the equalizer weights with these criteria requires computation of matrix inversion and the knowledge of the channel, which in most cases is not available. With this penalty function, the resulting target tap weights have been shown to be given by the Wiener filter, so that these algorithms may be viewed as an iterative approximation to the Wiener filter However, adaptive algorithms like LMS and RLS can be used to recursively update the equalizer weights during the training period.

Two adaptive methods which employ this least square error penalty function are the least mean square (LMS) and the more complex recursive least squares (RLS) algorithms. LMS algorithm is depicted schematically in Figure 4.8.

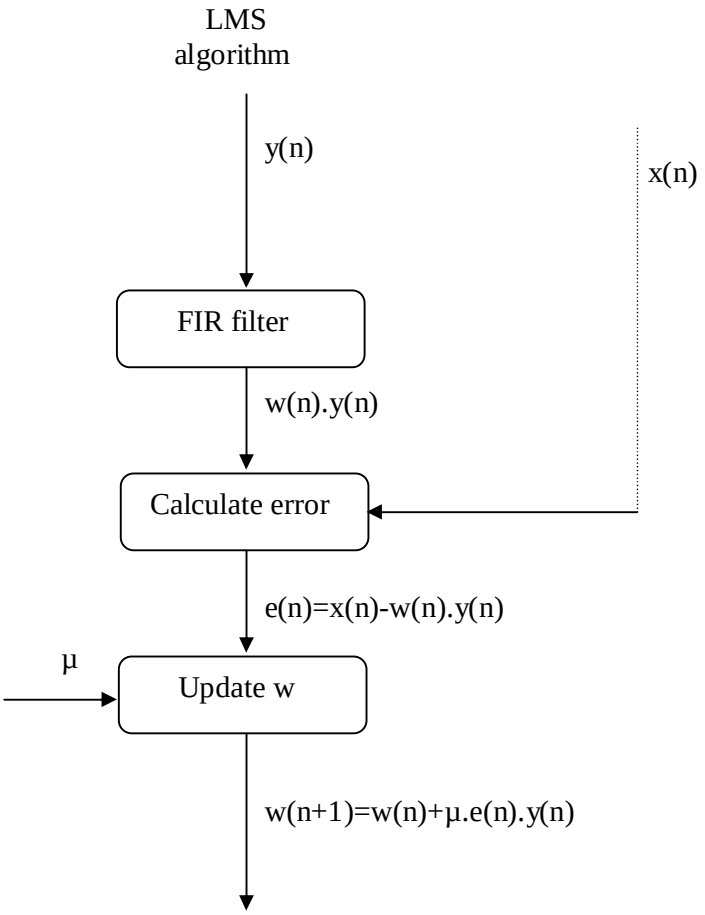


Figure 4.8 LMS algorithm

In LMS algorithm, correlation with an FIR filter is performed to obtain a (soft) estimate, $\hat{x}$, of the training data bit x(n) , as in the correlator receiver. The error e(n) in this estimate is then used to update the tap weights of the FIR receiver filter. In the LMS algorithm, this is performed by simple weighting of the error by step size μ.

4.5 SIMULATION RESULTS

In order to validate the proposed GA for DS-CDMA applications, extensive simulation studies were conducted. All the simulation studies were conducted on a 2.80 GHz PC with 512 MB of RAM with Microsoft windows XP operating system. All the simulations are done in Matlab. During the training period the receiver parameters were optimized/ trained with 1000 random samples and the parameters so obtained were averaged over 50 experiments. The parameters of the receiver were fixed after the training phase.

Bit error rate (BER) was considered as the performance index. In this section, the BER performance of the different linear receivers like matched filter and MMSE receiver using gold spreading sequences is done and the performance is compared with GA assisted

DS CDMA downlink receiver using gold sequences. In all the experiments randomly generated +1/-1 samples were transmitted for each user. In all the simulations, gold sequences of 31 chips are considered. These samples were spread using gold sequences of length 31 corresponding to each of the users. For comparison with gold sequences, the maximum permissible user's in the system is restricted to 31. After spreading, the sequences were added and transmitted through the non-dispersive channel. The channel corrupted the transmitted signal with AWGN. The channel output was fed to the various linear receiver structures like Matched filter and MMSE receiver. A total of 10^5 bits were transmitted by each user and a minimum of 1000 errors were recorded. The tests were conducted for different levels of SNR. Additionally tests were also conducted by varying number of active users in the system for fixed value of SNR.

4.5.1 Performance of different receivers for channel without ISI: - In this section, a non-dispersive channel is considered. In figure 4.9 the BER performance against the number of users of Matched filter is evaluated using gold sequences with 31 chips. Figure 4.9 is the BER performance of Matched filter receiver using gold sequences .The chip length of the gold codes are taken as 31 chips. Here SNR was fixed as 7dB .

In Figure 4.10 performance of matched filter receiver was investigated for varying SNR conditions. Performance for gold sequences for 4 and 7 users are plotted in Figure 4.10.

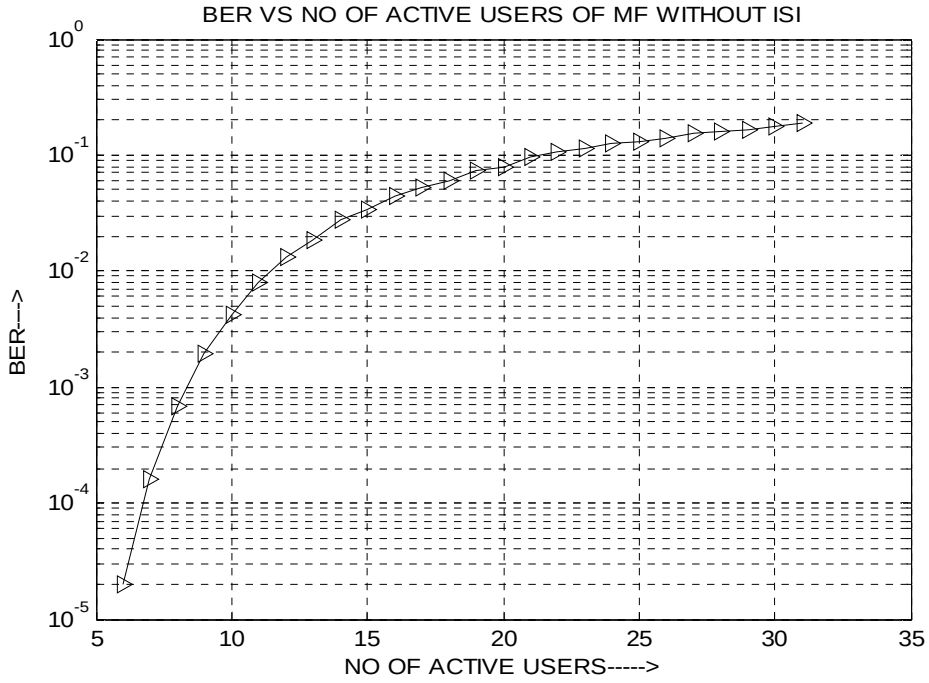


Figure 4.9: BER against the number of users of linear receivers in AWGN at SNR=7dB using gold sequences with 31chips.

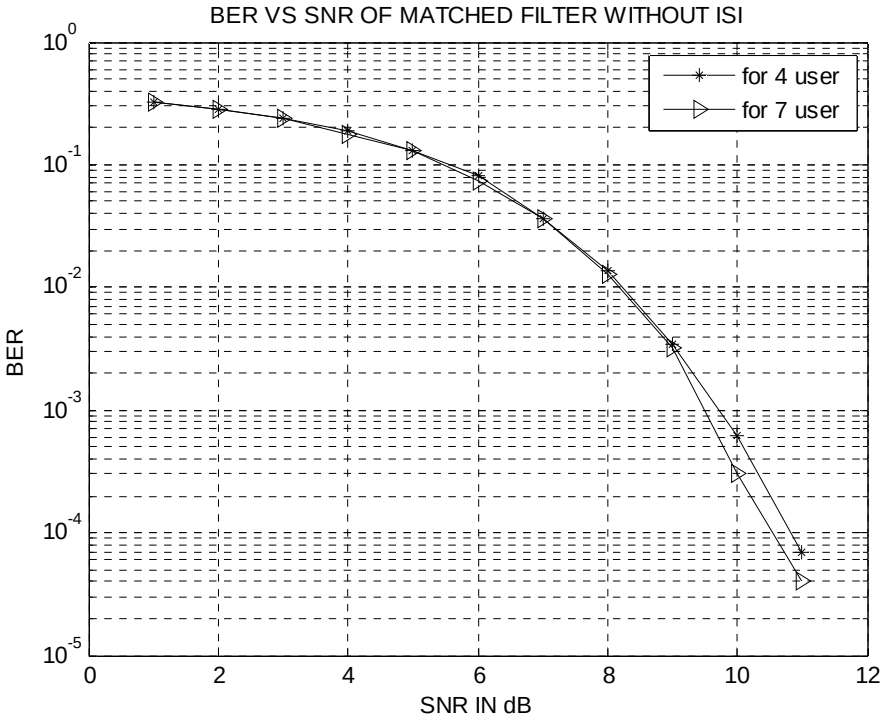


Figure 4.10 BER performance of Matched filter for varying SNR for 4 users and 7users being active in the system being active in the system in AWGN

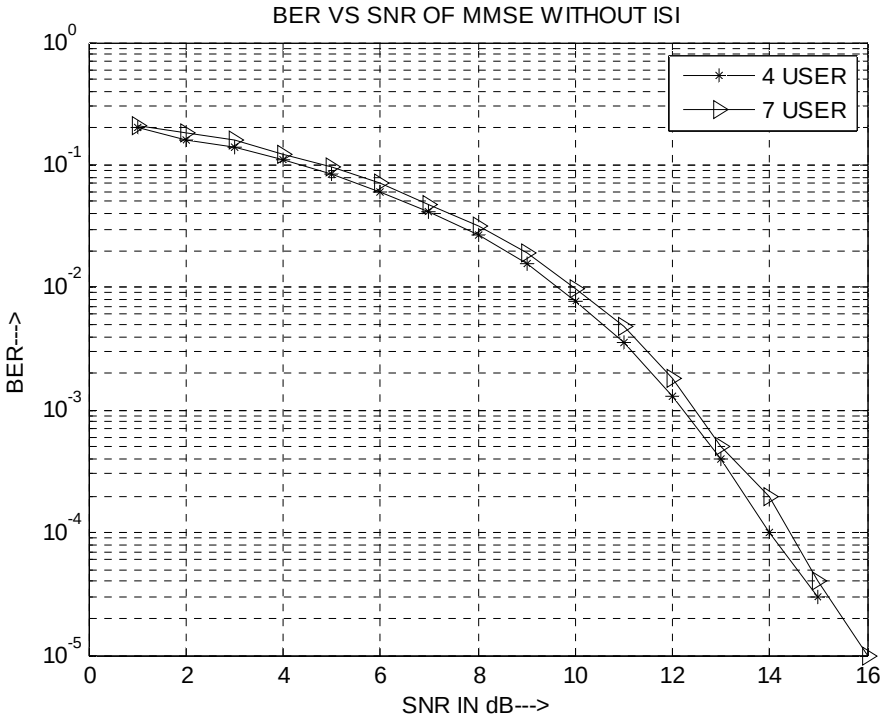


Figure 4.11 BER performance of MMSE receiver for varying SNR for 4 users and 7 users being active in the system in AWGN channel

In Figure 4.11 performance of MMSE receiver was investigated for varying SNR conditions. Performance for gold sequences for 4 and 7 users are plotted in Figure 4.11. In Figure 4.12 Performance of MMSE receiver was investigated for varying no of active users conditions.

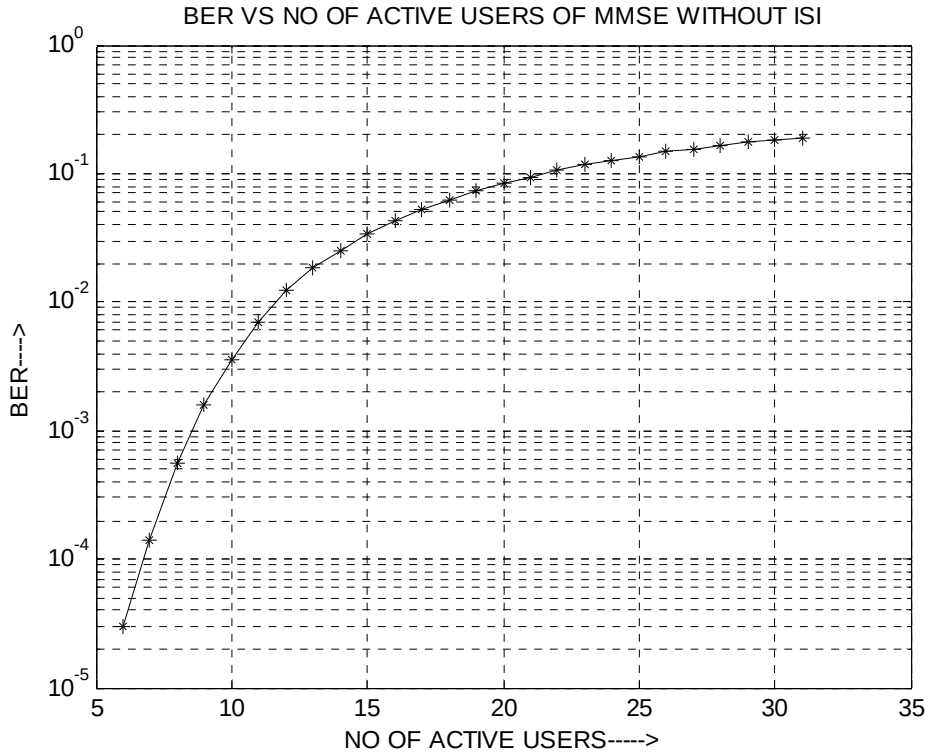


Figure 4.12 BER performance of MMSE receiver for varying no of active users in AWGN using gold codes with 31 chips

In Figure 4.13 performance of GA assisted DS CDMA receiver was investigated for varying SNR conditions. Performance for gold sequences for 4 and 7 users are plotted in Figure 4.13. In Figure 4.14 Performance of MMSE receiver was investigated for varying no of active users conditions. From the performance of all the receivers it is fact that when there is increase in no of users the performance of each receiver degrades i.e. when no of users are 4 the BER vs SNR plot shifts up when the no of user are 7.Similarly,from the plots of BER vs NO OF ACTIVE USERS it is seen that when the no of active users are less then the bit error rate is very less and in increasing the no of active user the bit error rate exponentially increases and approaches to 10^{-1}.

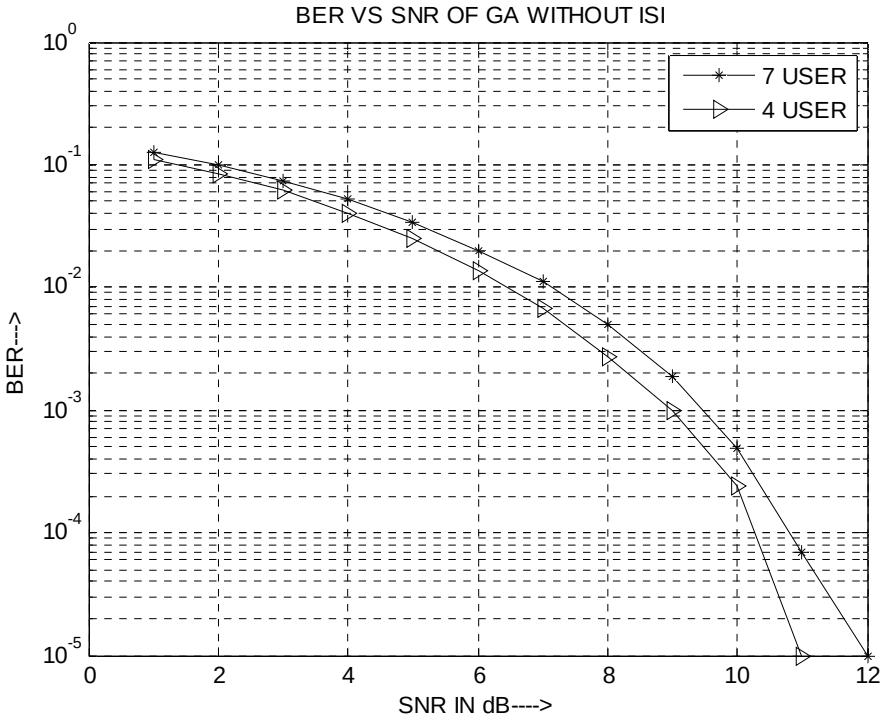


Figure 4.13 BER performance of GA assisted DS CDMA receiver for varying SNR for 4 users and 7 users being active in the system in AWGN channel

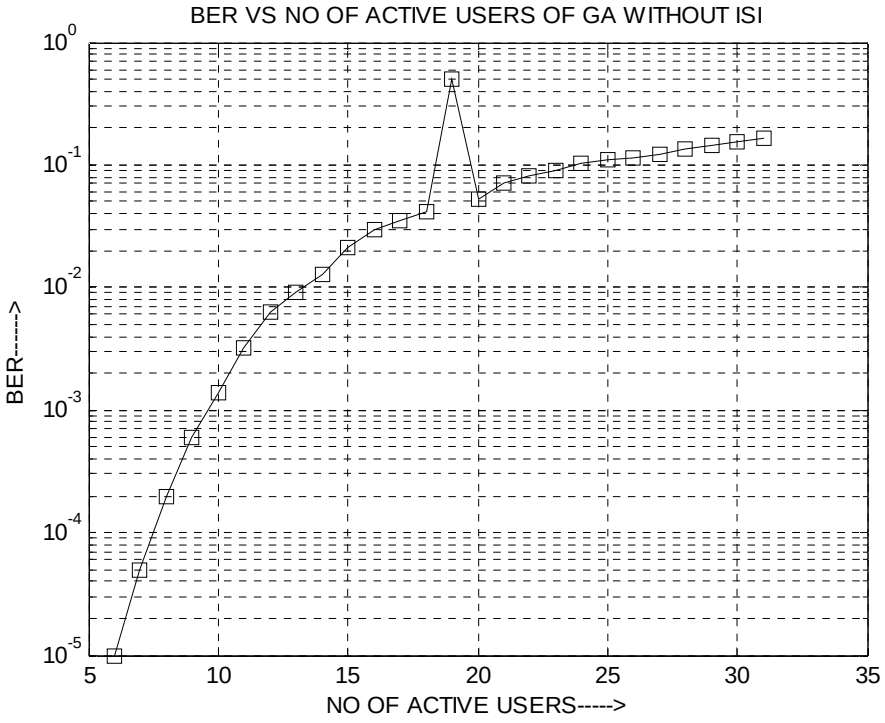


Figure 4.14 BER performance of GA assisted DS CDMA receiver for varying no of active users in AWGN using gold codes with 31 chips

4.5.2 Performance of different receivers for channel with ISI:- In this section , we consider a stationary multipath channel $H_{ch}=1+0.5z^{-1}+0.2z^{-2}$ .In AWGN the number of chips of transmitted is number of chips of the spreading sequence i.e., 31 in this case. In case of multipath channel, inter symbol interference (ISI) is induced from the previous and next symbol into account. So the number of chips will increase. Here, the multipath channel consists of 3 taps. Hence all receiver structures exploit N+ (L-1) = 31+ (3-1) = 33 chips instead of 31. Matched filter is used in AWGN channel whereas Rake receiver is used in Multipath channel.

In Figure 4.15 performance of matched filter receiver was investigated for varying SNR conditions. Performance for gold sequences for 4 and 7 users are plotted in Figure 4.15

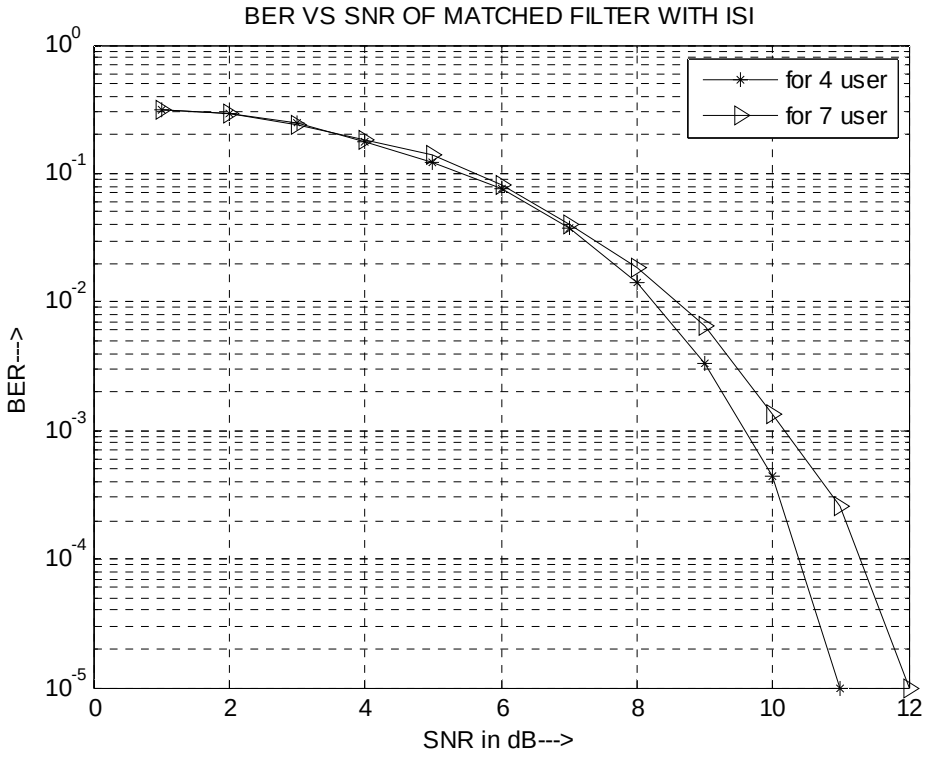
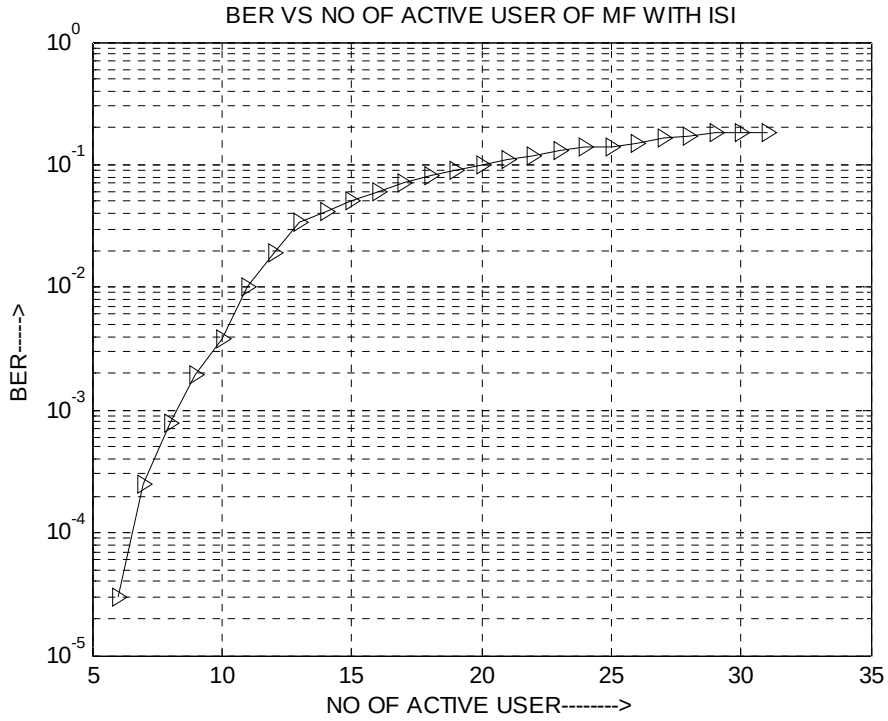


Figure: 4.15 BER performance of matched filter receiver for varying SNR for 4 and 7 users being active in the system in multipath channel $H_{ch}=1+0.5z^{-1}+0.2z^{-2}$

In Figure 4.16 performance of matched filter receiver was investigated for varying no of active users conditions with multipath channel. $H_{ch}=1+0.5z^{-1}+0.2z^{-2}$



4.16 performance of matched filter receiver was investigated for varying no of active users conditions with multipath channel. $H_{ch}=1+0.5z^{-1}+0.2z^{-2}$

In Figure 4.17 performance of MMSE receiver was investigated for varying SNR conditions. Performance for gold sequences for 4 and 7 users are plotted in Figure 4.17

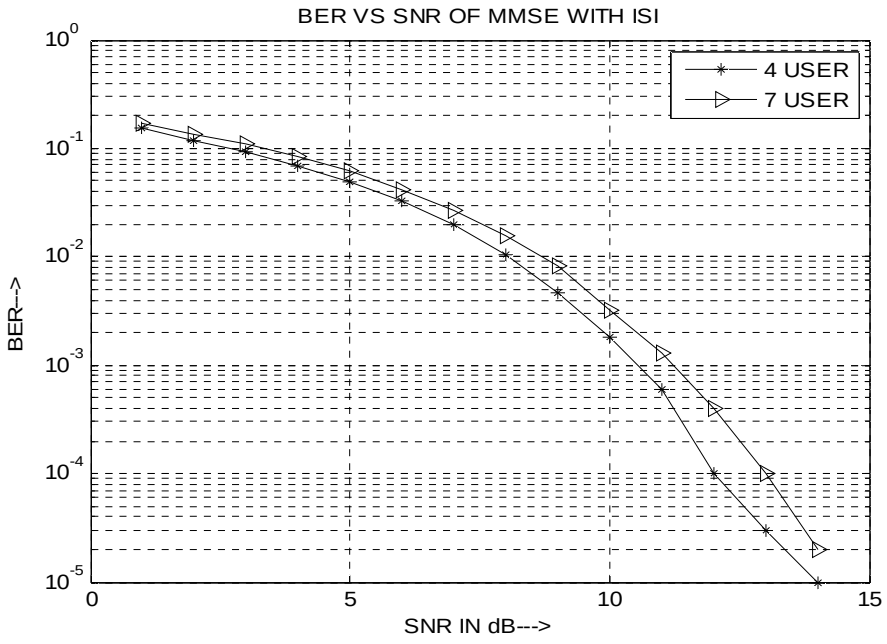


Figure: 4.17 BER performance of MMSE receiver for varying SNR for 4 and 7 users being active in the system in multipath channel $H_{ch}=1+0.5z^{-1}+0.2z^{-2}$

In Figure 4.18 performance of MMSE receiver was investigated for varying no of active users conditions with multipath channel. $H_{ch}=1+0.5z^{-1}+0.2z^{-2}$ using gold codes.

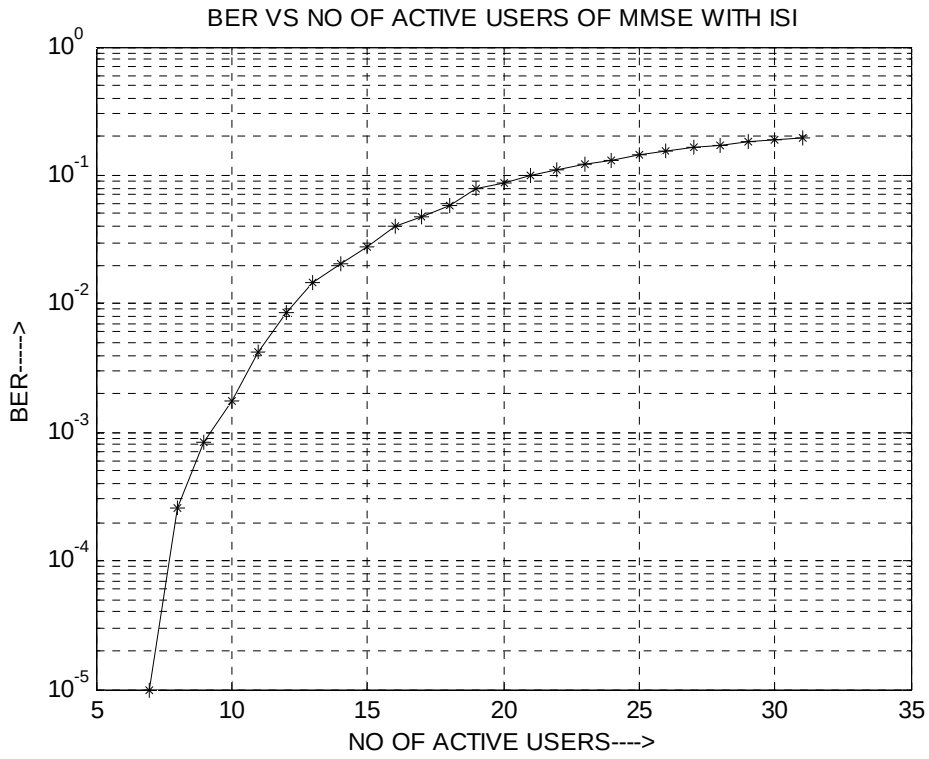


Figure 4.18 performance of MMSE receiver was investigated for varying no of active users conditions with multipath channel. $H_{ch}=1+0.5z^{-1}+0.2z^{-2}$ using gold codes.

In Figure 4.19 BER performance of RAKE receiver using gold sequences was investigated. The chip lengths of both the gold codes are taken as 31 chips. Here SNR was fixed as 7dB .In Figure 4.20 BER performance of RAKE receiver using gold sequences for 4 user and 7 user was investigated .The chip lengths of both the gold codes are taken as 31 chips. Here SNR was varied from 0 to 15.In Figure 4.21 BER performance of GA assisted CDMA receiver using gold sequences for 4 user and 7 user was investigated .The chip lengths of both the gold codes are taken as 31 chips. Here SNR was varied from 0 to 15. In Figure 4.22 BER performance of GA assisted CDMA receiver using gold sequences was investigated .The chip lengths of both the gold codes are taken as 31 chips. Here SNR was fixed as 7dB. From the performance of all the receivers it is fact that when there is increase in no of users the performance of each receiver degrades i.e. when no of users are 4 the BER vs SNR plot shifts up when the no of user are 7.Similarly,from the plots of BER vs NO OF ACTIVE USERS it is seen that when the no of active users are less then the bit error rate is very less and in increasing the no of active user the bit error rate exponentially increases and approaches to 10^{-1}.

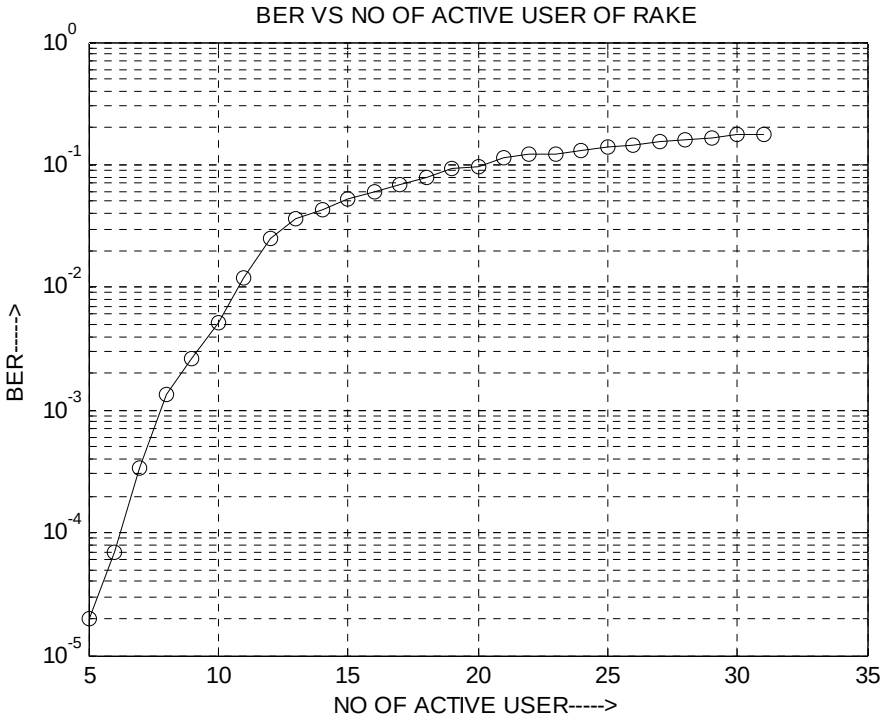


Figure 4.19: BER against the number of users of RAKE receiver in AWGN at SNR=7dB using gold sequences with 31chips in multipath channel $H_{ch}=1+0.5z^{-1}+0.2z^{-2}$

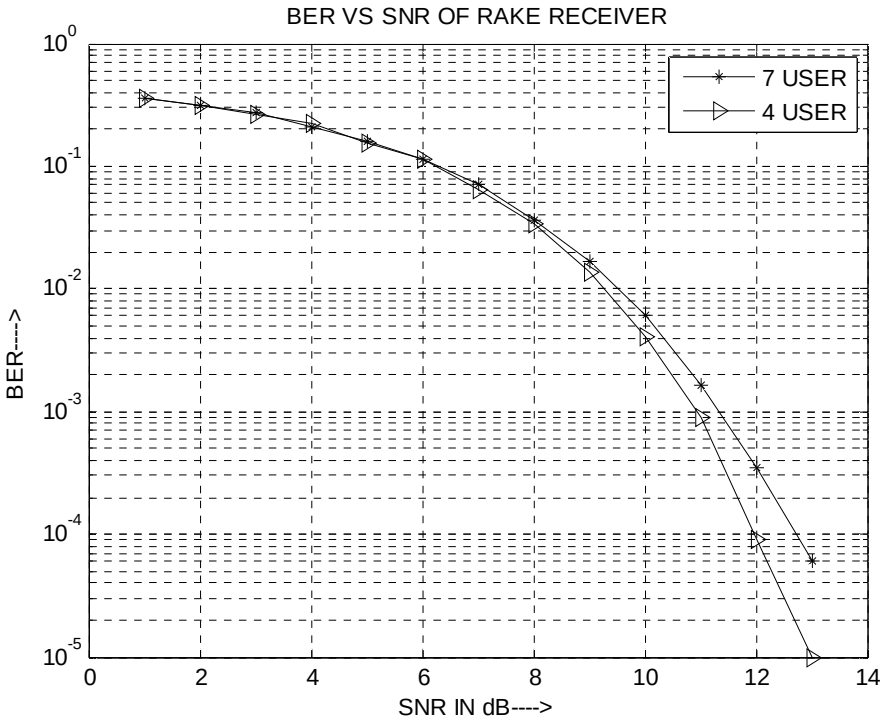


Figure: 4.20 BER performance of RAKE receiver for varying E_b/N_0 for 4 and 7 users being active in the system in multipath channel $H_{ch}=1+0.5z^{-1}+0.2z^{-2}$

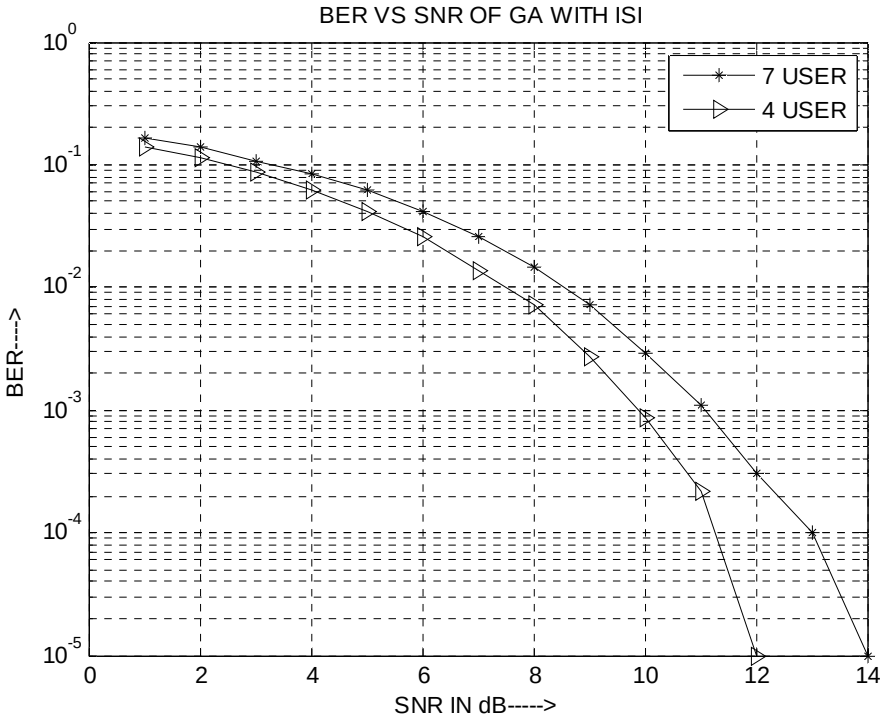


Figure 4.21 BER performance of GA assisted CDMA receiver using gold sequences for 4 user and 7 user being active in the system in multipath channel $H_{ch}=1+0.5z^{-1}+0.2z^{-2}$

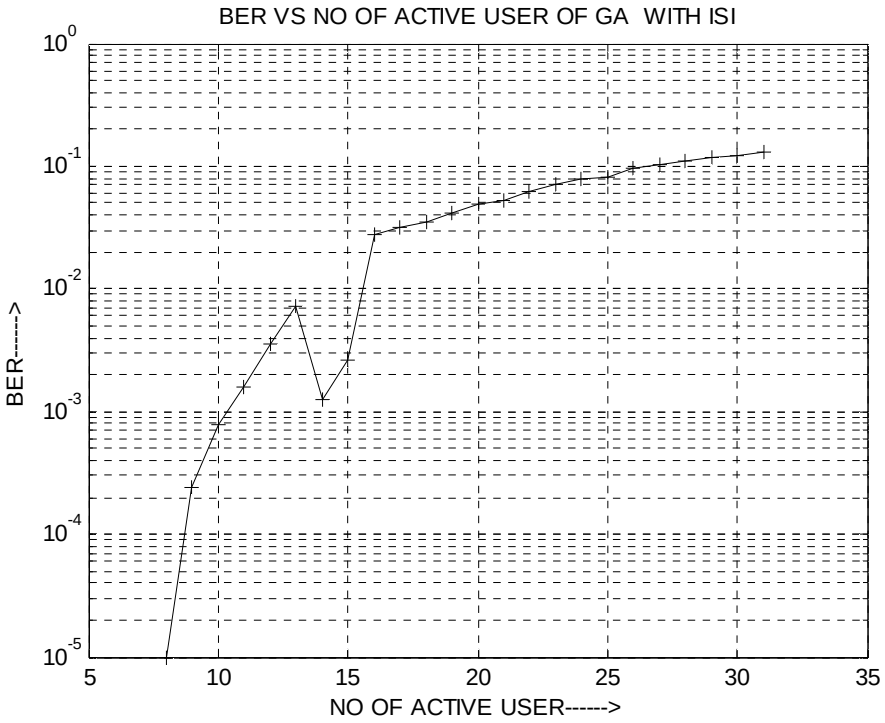


Figure 4.22: BER against the number of users of GA assisted CDMA receiver in AWGN at SNR=7dB using gold sequences with 31chips in multipath channel $H_{ch}=1+0.5z^{-1}+0.2z^{-}$

4.5.3 Performance comparison of different receivers for channel without ISI: - In this section, a non-dispersive channel is considered. In figure 4.23 the BER performance against the number of users is evaluated using gold sequences with 31 chips. Figure 4.23 is the BER performance of different receivers using gold sequences .The chip length of the gold codes are taken as 31 chips. Here SNR was fixed as 7dB .

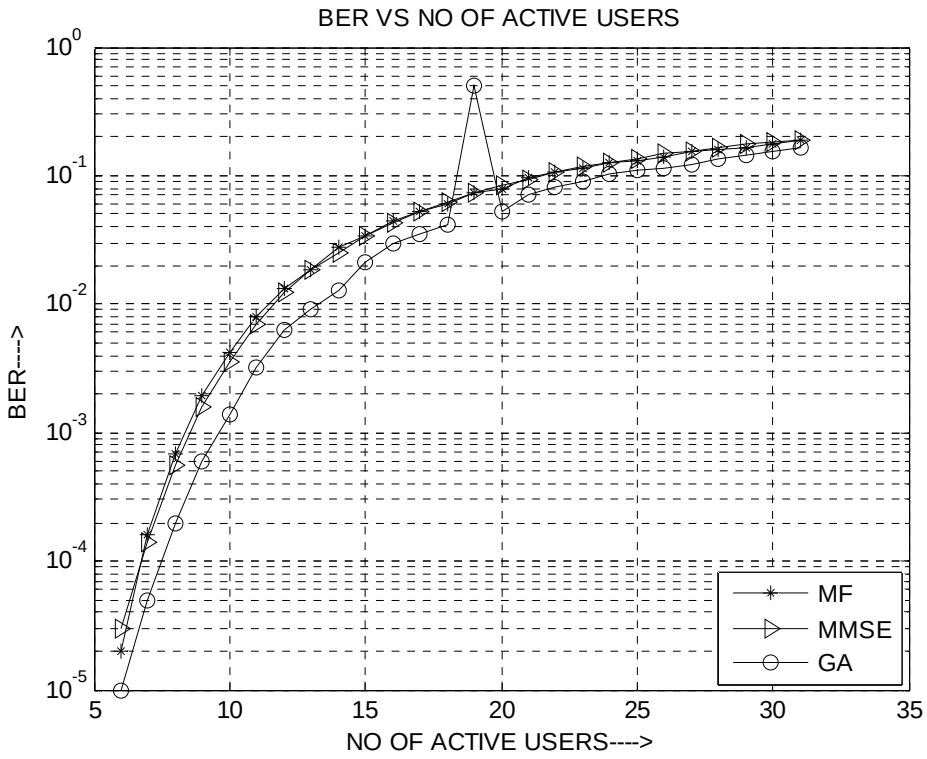


Figure 4.23: BER against the number of users of linear receivers in AWGN at SNR=7dB using gold sequences with 31chips .

In figure 4.23 it is seen that matched filter receiver and MMSE receiver have closely almost same performance but GA assisted CDMA receiver very good performance over the other two receivers. When BER=10^{-5} then in GA assisted CDMA receiver no of users=6.At same no of users (i.e. no of users=6) the matched filter has BER=$10^{-4.9}$ and MMSE has BER=$10^{-4.8}$.

In Figure 4.24 performance of different receivers were investigated for varying SNR conditions. Performance gold sequences for 4 users are plotted in Figure 4.24. It is seen that when the number of users is 4, there is a 1dB performance difference at a BER of 10^{-5} between GA assisted CDMA receiver and the matched filter receiver, and 5 dB performance difference between GA assisted CDMA receiver and MMSE receiver .

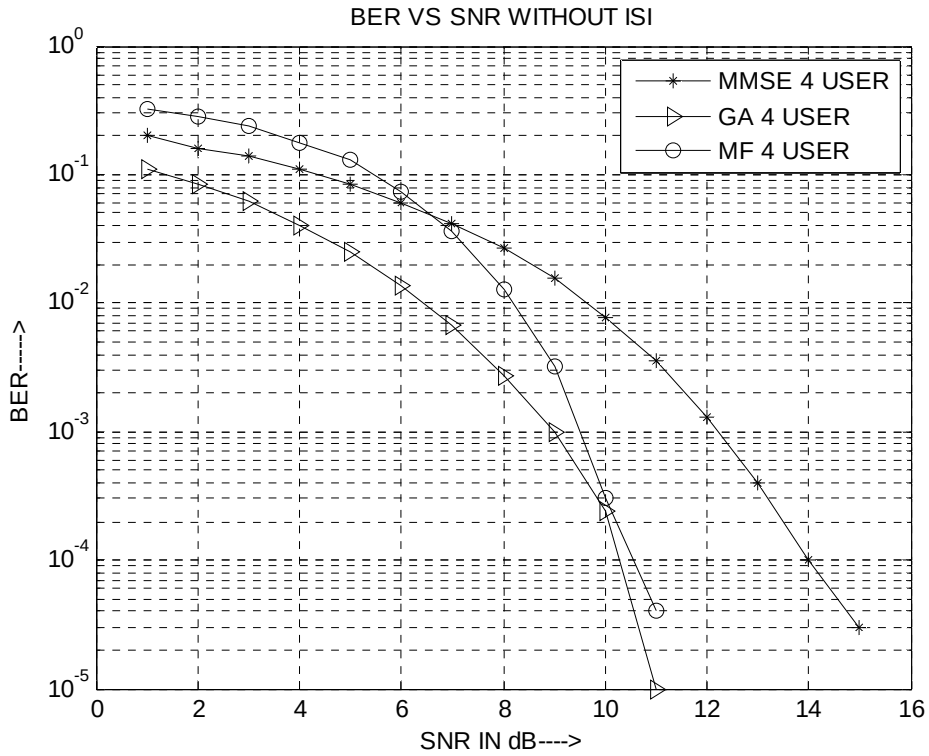


Figure 4.24: BER performance of different receivers for varying SNR for 4 users being active in the system.

4.5.4 Performance comparison of different receivers for channel with ISI:- In this section, we consider a stationary multipath channel $H_{ch}=1+0.5z^{-1}+0.2z^{-2}$ .In AWGN the number of chips of transmitted is number of chips of the spreading sequence i.e., 31 in this case. In case of multipath channel, inter symbol interference (ISI) is induced from the previous and next symbol into account. So the number of chips will increase. Here, the multipath channel consists of 3 taps. Hence all receiver structures exploit N+ (L-1) = 31+ (3-1) = 33 chips instead of 31. Matched filter is used in AWGN channel whereas Rake receiver is used in Multipath channel.

Figure 4.25 is the BER performance of different receivers using gold sequences .The chip lengths of the gold codes are taken as 31 chips. Here SNR was fixed as 7dB and the multipath channel $H_{ch}=1+0.5z^{-1}+0.2z^{-2}$. In Figure 4.26 performance of different receivers were investigated for varying SNR conditions and the multipath channel $H_{ch}=1+0.5z^{-1}+0.2z^{-2}$. Performance gold sequences for 4 users are plotted in Figure 4.26.

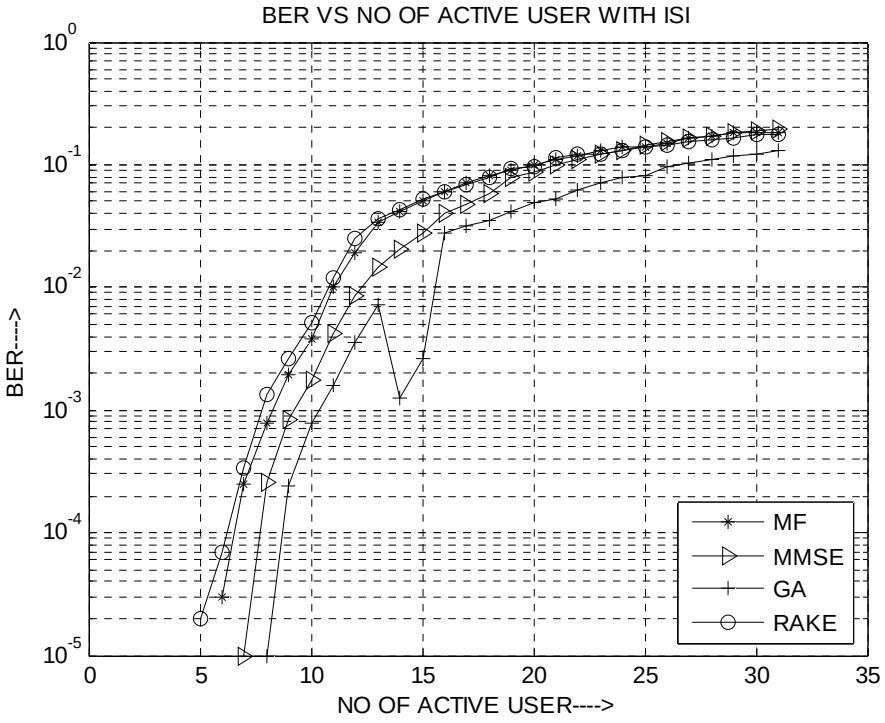


Figure 4.25: BER performance of different receivers for varying no of active users being active in the system in multipath channel $H_{ch}=1+0.5z^{-1}+0.2z^{-2}$

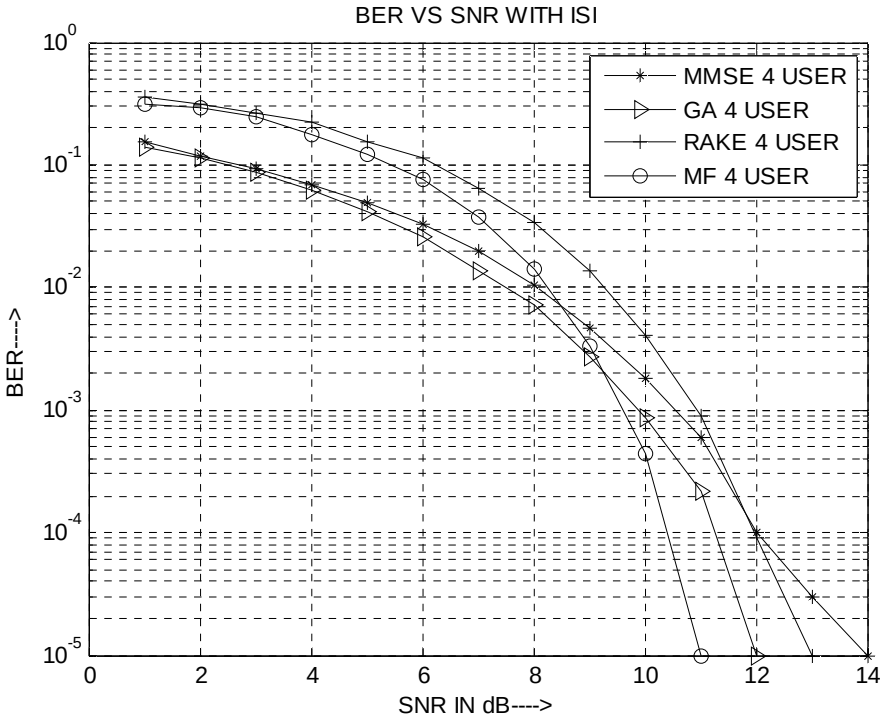


Figure 4.26: BER performance of different receivers for varying SNR for 4 users being active in the system in multipath channel $H_{ch}=1+0.5z^{-1}+0.2z^{-2}$

In figure 4.25 it is seen that matched filter receiver and RAKE receiver have closely almost same performance but MMSE gives better performance than previous two. Again GA assisted CDMA receiver gives best performance among the four receivers. At BER=10^{-5} the no of users in RAKE is 5 ,the no of users in matched filter is 6 while no of user in MMSE is 7 and in GA assisted CDMA receiver no of users is 8.

In Figure 4.26 performance of different receivers were investigated for varying SNR conditions. Performance gold sequences for 4 users are plotted in Figure 4.26. It is seen that when the number of users is 4, there is a 1dB performance difference at a BER of 10^{-5} between GA assisted CDMA receiver and the matched filter receiver and also for RAKE receiver, and 2 dB performance difference between GA assisted CDMA receiver and MMSE receiver

4.6 CONCLUSION

In this chapter various linear receivers like Matched filter, MMSE receiver and RAKE receiver is explained. BER performance of different linear receivers using gold sequences is evaluated. It is seen that GA based DS-CDMA receiver performs much better than other type of receivers.

Chapter 5

CONCLUSIONS

5. CONCLUSIONS

5.1 INTRODUCTION

In this thesis a new type of DS-CDMA receiver was investigated called GA assisted DS CDMA receiver. The performance of different receiver techniques were evaluated and compared with GA based DS CDMA receiver using gold code . This chapter summarizes the work reported in this thesis, specifying the limitations of the study and provides some indications for future work.

Following this introduction section 5.2 lists the achievements from the work. Section 5.3 provides the limitations and section 5.4 presents indications toward future work.

5.2 ACHIEVEMENT OF THE THESIS

In chapter 3, principle of Genetic Algorithm has been discussed. In Chapter 4, various linear receivers like Matched filter, MMSE receiver etc., are studied and BER performance of different linear receivers using gold sequences are evaluated and are compared with the receivers using GA and gold sequences. It is seen that GA based DS-CDMA performs than the other type of receivers. The results also showed that MMSE receiver performs better than RAKE receiver.

5.3 LIMITATIONS OF THE THESIS

- Simulations are constrained to baseband only.
- Fading effects is not considered.
- Spreading codes with only 31 length is considered.
- The work investigated in this thesis investigates the receiver in the downlink scenario only.

5.4 SCOPE OF FURTHER RESEARCH

- Simulations can be extended to some more nonlinear receivers like neural network receivers.
- Faster convergence of GA based CDMA receiver can also be investigated.
- Simulations can be extended to larger spreading codes like 63,127 chip etc.,

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